

**Amendments to the Specification:**

Please replace the paragraph beginning at page 1, line 4, with the following:

The present application claims priority to USSN 60/421,989, filed October 29, 2002, and USSN 60/\_\_\_\_\_512,251, TTC Ref. No. ~~021044-005810~~, filed October 17, 2003, each herein incorporated by reference in their entirety.

Please replace the paragraph beginning at page 4, line 23, with the following:

--Figure 14 shows that Axl RNAi reduces Axl protein expression. Axl 2 = SEQ ID NOS:61 and 62; Axl-2 = SEQ ID NO:63; Axl2 = SEQ ID NO:64; Axl4 = SEQ ID NOS:65 and 66; Axl4.2 = SEQ ID NOS:67 and 68; Axl-4 = SEQ ID NO:69; Axl4 = SEQ ID NO:70; Axl4.2 = SEQ ID NO:71.--

Please replace the paragraph beginning at page 11, line 15, with the following:

--The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same (i.e., about 70% identity, preferably 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region (e.g., ~~SEQ ID NO:1 or 2~~ SEQ ID NO:3 or 4), when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the compliment of a test sequence. The definition also includes sequences that have deletions and/or additions, as

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well as those that have substitutions. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.--

Please replace the paragraph beginning at page 38, line 8, with the following:

--Common linkers such as peptides, polyethers, and the like can also serve as tags, and include polypeptide sequences, such as poly gly Gly sequences of between about 5 and 200 amino acids (SEQ ID NO:72). Such flexible linkers are known to persons of skill in the art. For example, poly(ethylene glycol) poly(ethylene glycol) linkers are available from Shearwater Polymers, Inc. Huntsville, Alabama. These linkers optionally have amide linkages, sulfhydryl linkages, or heterofunctional linkages.--

Please replace the informal "SEQUENCE LISTING at pages 50-78 with the following:

--SEQUENCE LISTING

Ax1

GH2\_420\_G3F1 (SEQ ID NO:1)

CTCCAGGGGTTCAAGATAACCTCACCCTCATCCATGTTGACATAGAGGATTTCGTCAAGGCTCTGGCAGGAGGCA  
AGG

GH2\_420\_G3R1 (SEQ ID NO:2)

ATCTATCTAACCACTGTGCTGGGTTCTGGCCCTTGCCCTGCCAGGAGCCTGACGAAATCCTCTATGTCAACA  
TGGATGAGGGTGGAGGTTATCCTGAACCCCTGGAG

>gi|21536465|ref|NM\_021913.2| Homo\sapiens AXL receptor tyrosine kinase  
(AXL), transcript variant 1, mRNA (SEQ ID NO:3)

GAGTGGAGTCTGGAGGAATGTTTACCAAGACACAGAGCCCCAGAGGGACAGCGCCCAGAGCCCAGATAGAG  
AGACACGGCCTCACTGGCTCAGCACCAAGGGTCCCTCCCTCCCTCAGCTCCCTCCCTGGCCCTTTAA  
GAAAGAGCTGATCCTCCTCTTGAGTTAACCCCTGATTGTCCAGGTGGCCCTGGCTCTGGCCTGGT  
GGCGGGAGGCAAAGGGGGAGCCAGGGCGGAGAAAGGTTGCCAAGTCTGGAGTGAGGAAGGAGGCA  
GGGTGCTGAGAAGGCGGCTGCTGGCAGAGCCGGTGGCAAGGGCCTCCCTGCCGCTGTGCCAGGCAGG  
CAGTCCAATCCGGGAGCCTGGAGCTGGGGGAGGCCGGGACAGCCGGCCCTGCCCTCCCCCG  
CTGGGAGCCAGCAACTCTGAGGAAAGTTGGCACCCATGGCGTGGCGGTCCCCCAGGATGGCAGGGT

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CCCGCTGGCCTGGTCTGGCGCTGTGCGGCTGGCGTGCATGCCCCCCAGGGCACCGAGGCTGAAGAA  
AGTCCCTTCGTGGCAACCAGGAATATCACAGGTGCCGGACTCACGGCACCCCTCGGTGTCAGC  
TCCAGGTTCAGGGAGAGCCCCCGAGGTACATTGGCTCGGGATGGACAGATCCTGGAGCTCGCGACAG  
CACCCAGACCAGGTGCCCTGGGTGAGGATGAACAGGATGACTGGATAGTGGTCAGCAGCTCAGAATC  
ACCTCCCTGCAGCTTCCGACACGGGACAGTACAGTGTGTTCTGGACATCAGACCTCGTGT  
CCCAGCCTGGCTATGTGGCTGGAGGGCTGCCTACTTCCTGGAGGAGCCGAAGACAGGACTGTGGC  
CGCCAACACCCCTTCACACTGAGCTGCCAAGCTCAGGGACCCCCAGAGCCGTGGACCTACTCTGGCTC  
CAGGATGCTGTCCCCCTGGCCACGGCTCCAGGTACGGCCAGCGCAGCCTGCATGTTCCAGGGCTGA  
ACAAGACATCCTCTTCTCGCAAGGCCATAACGCCAAGGGGTCAACCACATCCCGCACAGCCACCAT  
CACAGTGCTCCCCCAGCAGCCCCGTAACCTCCACCTGGTCTCCGCCAACCCACGGAGCTGGAGGTGGCT  
TGGACTCCAGGCCCTGAGCGCATCTACCCCTGACCCACTGCACCCCTGCAGGCTGTGCTGTCAGACGATG  
GGATGGGCATCCAGGGGAGAACCCAGACCCCCCAGAGGAGCCCTCACCTCGCAAGCATCCGTCCCCC  
CCATCAGCTCGGCTAGGCAGCCTCCATCCTCACACCCCTTATCACATCCCGTGGCATGCAACCAGCAGC  
CAGGGCCCTCATCCTGGACCCACTGGCTTCTGTGGAGACGCCGGAGGGAGTGCCCTGGGCCCTG  
AGAACATTAGTGTACCGGAATGGAGCCAGGCCCTCGTGCATGGCAAGAGCCGGGCGCCCTGCA  
GGTACCTGTTAGGGTACCGGCTGGCGTATCAAGGCCAGGACACCCCAGAGGTGCTAATGGACATAGGG  
CTAAGGCAAGAGGTGACCCCTGGAGGCTGCAGGGGACGGGCTGTGTCATGACAGTGTGTGGCAG  
CCTACACTGCTGCTGGGATGGACCCCTGGAGCCTCCAGTACCCCTGGAGGCGCTGGGCCAGGGCAAGC  
ACAGCCAGTCCACCAGCTGGTAAGGAACCTCAACTCCTGCCTCTCGTGGCCCTGGTGGTATGACTG  
CTAGGAGCAGTCGTGGCGCTGCTGTCTCATCTGGCTCTTCCTGTCCACCGCGAAAGAAGG  
AGACCCGTTATGGAGAAGTGTGTTGAACCAACAGTGGAAAGAGGTGAAGTGGTAGTCAGGTACCGCGTGC  
CAAGTCCTACAGTCGCGGACCACTGAAGCTACCTGAACAGCCTGGGCATCAGTGAAGAGCTGAAGGAG  
AAGCTCGGGGATGTGATGGTGGACCGGCACAAGGTGGCCTGGGAAGACTCTGGGAGAGGAGAGTTG  
GAGCTGTGATGGAAGGCCAGCTCAACCAGGACACTCCATCCTCAAGGTGGCTGTGAAGACGATGAAGAT  
TGCATCTGCACGAGGTCAAGAGCTGGAGGATTCTCTGAGTGAAGCGGCTGCTGATGAAGGAATTGACCAT  
CCCAACGTCATGAGGCTCATCGGTGCTGTGTTCCAGGGTTCTGAACGAGAGCTCCAGCACCTGTGG  
TCATCTTACCTTCATGAAACATGGAGACCTACACAGCTCCTCTCATTCGGGCTCGGGGACAGCC  
AGTGTACCTGCCACTCAGATGCTAGTGAAGTTCATGGCAGACATGCCAGTGGCATGGAGTATCTGAGT  
ACCAAGAGATTACACCCGGACCTGGCGGCCAGGAACCTGCATGCTGAATGAGAACATGTCCGTGTG  
TGGCGGACTCGGGCTCTCCAAGAAGATCTACAATGGGACTACTACCGCCAGGGACGTATGCCAAGAT  
GCCAGTCAGTGGATTGCCATTGAGAGTCTAGCTGACCGTGTCTACACCAGCAAGAGCGATGTGGTCC  
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TTATGACTATCTGCCAGGGAAATCGCCTGAAGCAGCCTGCGACTGTCTGGATGGACTGTATGCC  
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AACACACTGAAGGCCTGCCCTGCCAGGAGCCTGACGAATCCTCTATGTCACATGGATGAGGGTG  
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CTGTAGCTGCCCACTCGGGCTGAGGTCCATCCTGCTGGACGCTATGTCCTCTGCCCTCCACAACCCCT  
AGCCCCGCTCAGCCTGCTGATAGGGCTCCCAGCAGCCCCAGGGCAGGAGGATGGTGCCTGAGACAACC  
CTCCACCTGTTACTCCTCTCAGGATCCAAGCTAAGCACTGCCACTGGGAAAACCTCCACCTCCACTT  
TCCCACCCACGCCCTATCCCCACTGCAAGCCCTGTCTCTCACCTATCCCACCTCCACAGACAGGT  
CCCTCCCTCTCTGTCAGTACCATCACCTGAAAGCAGTAGCATCACCATCTGTAAGGAAGGGTT  
GGATTGCAATATCTGAAGCCCTCCAGGTGTTAACATCCAAGACTCTAGAGTCCAAGGTTAAAGAGTC  
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TGACCTCAAGTGTACTGCCACCTCAGCCTCCAAAGTGTGAGGATTACAGGACATGAGGCCACTGCACTCA  
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TAAAGCCTCAAGGTTTAGGTTCTAAAGTCTAAAGATTCTGATTAGGAGCTAAGGCTCTATGAGTCTA  
GATGTTATTCTCTAGAGTTCAGAGTCCTAAAGATTAGATTCTAAAGATTCTATAGTTCT  
AGACATGGAGGTTCTAAGGCCTAGGATTCTAAAGTGTGATGTTCTAAGGCTCTGAGAGTCTAGATTCTCT

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GGCTGTAAGGCTCTAGATCATAAGGCTCAAAATGTTATCTTCTCAAGTTCTAAGATTCTAATGATGATC  
 AATTATAGTTCTGAGGCTTATGATAATAGATTCTCTGTATAAGATCCTAGATCCTAAGGGTCGAAAG  
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 GTGATATTCTAAGACTACTCTAAGATCTTAGATTCTCTGTCTAAGATTCTAGATCAGATGCTCCAAG  
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 GTTTCTAAGATTCTAAAGGTCCACAGGTCTAGACTATTAGGTGCAATTCAAGGTCTAACCTTAACTG  
 TAGTATTCTTGGGGTCCCCCTCCTCTAGCTATCATTGCTCCTCCCCAACTGTGGGGTGTG  
 CCCCCTCAAGCCTGTGCAATGCATTAGGGATGCCTCTTCCCCCAGGGGATGGACGATCTCCCACCTT  
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>gi|21536466|ref|NP\_068713.2| AXL receptor tyrosine kinase isoform 1; AXL transforming sequence/gene; oncogene AXL [Homo sapiens] (SEQ ID NO:4)  
 MAWRCPRMGRVPLAWCLALCGWACMAPRGTQAEESPFGNPGNITGARGLTGLRCQLVQGEPPVHWL  
 RDGQILELADSTQTQVPLGEDEQDDWIVVSQRLRITSQQLSDTGQYQCLVFLGHQTFVSQPGYVGLELPY  
 FLEEPEDRTVAANTPFNLSCQAQGPPEPVDLLWLQDAVPLATAPGHGPQRSLHVPGLNKTSSFSCEAHNA  
 KGVTTSRTATITVLPQQPRNLHLVRSPTELEVAWPGLSGIYPLTHCTLQAVLSDDGMGIQAGEPDPP  
 EPLTSQASVPPHQRLGLSLHPHTPYHIRVACTSSQGPSSWTHWLPVETPEGVPLGPENISATRNGSQAF  
 VHWQEPRAPLQGTLLGYRLAYQGQDTPEVLMIDIGLRQEVTLQGDGSVSNLTVCAAYTAAGDGPWSLP  
 VPLEAWRPQQAQPVHQLVKEPSTAFAFWPWYVLLGAVVAAACVLILALFLVHRRKKETRYGEVFEPTVE  
 RGELEVRYVRKSYSRRTTEATLNSLGISEELKEKLDRVMVDRHKVALGKTLGEGEFGAVMEQLNQDDS  
 ILKVAVKTMKIAICTRESEDFLSEAVCMKFDPNVMRMLIGVCQGSERESFPAPVVIILPFMKHDLHS  
 FLLYSRLGDQPVYLPTQMLVKFMADIASGMELYSLTRFIHRDLAARNCMLENMSVCVADFGLSKIYNG  
 DYRQGRIAKMPVKWIAIESLADRVTSKSDVWSFGVTMWEIATRGQTYPGVENSEIYDYLRQGNRLKQ  
 PADCLDGLYALMSRCWELNPQDRPSFTELREDLENTLKALPPAQEPDEILYVNMDEGGGYPEPPGAAGGA  
 DPPTQPDPKDSCSCLTAAEVHPAGRYVLCPTTPSAQPADRGSPAAPGQEDGA

>gi|21536467|ref|NM\_001699.3| Homo sapiens AXL receptor tyrosine kinase (AXL), transcript variant 2, mRNA (SEQ ID NO:5)  
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 GAAAGAGCTGATCCTCTCCTCTTGAGTTAACCCCTGATTGTCCAGGTGGCCCTGGCTCTGGCCTGGT  
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 CACAGTGCTCCCCCAGCAGCCCCGTAACCTCCACCTGGTCTCCCCCAACCCACGGAGCTGGAGGTGGCT  
 TGGACTCCAGGCTGAGCGGCATCTACCCCTGACCCACTGCACCTGCAGGCTGTGCTGTCAGACGATG  
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CAGGGCCCCCTCATCCTGGACCCACTGGGTTCCCTGTGGAGACGCCGGAGGGAGTCCCCCTGGGGCCCCCTGAGAACATTAGTGCTACGCAGGAAATGGGAGGCCAGGCCTTCGTGCATTGGCAAGAGCCCAGGGCGCCCCCTGCA  
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CCTTAAATGTAAGATTAGATTCTAAAGATTCTATAGTTCTAGACATGGAGGTCTAAGGCCCTAGGAT  
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TCAAAATGTTATCTCAAGTTCTAACATTGATGATCAATTATAGTTCTGAGGCTTATGATA  
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CGGTCTGTTCTGTTCAAGGCCACTCTAGATTCCATTGGCTAACAGATTCCGGATCTAACGATCTAACGG  
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TTATAGTTCTAGGACTGTTCTAACAGACTAACATTGTTCTAACAGATTCTAACGGTCTAACGG  
TCTAGACTATTAGGTGCAATTCAAGGTTCTAACCCCTAACACTGTTAGTATTCTTGGGGTGCCTCTCCT  
TCTTAGCTATGCTTCCCTCCCCAACGGTGGGGTGTGCCCCCTCAAGGCTGTGCAATGCATT  
GGGATGCCCTCTTCCCGCAGGGGATGGACGATCTCCACCTTCCGGGCTATGTTGCCCCCTGAGCCAA  
TCCCTCACCTCTGAGTACAGAGTGTGGACTCTGGTGCCTCCAGAGGGCTCAGGTACATAAAATTTG  
TATATCAACGAAAAAAA

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>gi|21536468|ref|NP\_001690.2| AXL receptor tyrosine kinase isoform 2; AXL transforming sequence/gene; oncogene AXL [Homo sapiens] (SEQ ID NO:6)  
MAWRCPRMGRVPLAWCLALCGWACMAPRGTQAEESPFGNPGNITGARGLTGTLRCQLQVQGEPPVHWL  
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FLEEPEDRTVAANTPFNLSCQAQGPPEPVDLLWLQDAVPLATAPGHGPORSLHVPGLNKTSSFSCEAHNA  
KGVTTSRTATITVLPQQPRNLHLVSRQPTELEVAWTPLSGIYPLTHCTLQAVLSDDGMGIQAGEPDPE  
EPLTSQASVPPHQRLGLSLHPHTPYHIRVACTSSQGPSSWTHWLPVETPEGVPLGPENISATRNGSQAF  
VHWQEPRAPLQGTLLGYRLAYQGQDTPEVLM DIGLRQEVTL ELQGDGSVSNLTVCAAYTAAGDGPWSLP  
VPLEAWRPVKEPSTPAFWSPWVYLLGAVVAAACVLILALFLVHRRKKETRYGEVFEPTVERGELVVRYR  
VRKSYSRRTTEATLNSLGISEELKELRDVMVDRHKVALGKTLGEGEFGAVMEGQLNQDDSILKAVAKTM  
KIAICTRSELEDFLSEAVCMKEFDHPNVMRLIGVCFQGSERESFPAPVVLIPFMKHGDLHSFLYSRLGD  
QPVYLPTQMLVKFMADIASGMEYLSTKRFIHRDLAARNCMLNEAMSVCADFLSKKIYNGDYYRQGRIA  
KMPVKWIAIESLADRVYTSKSDVWSFGVTMWEIATRGQTYPGVENSEIYDYLQRQGNRLKQPADCLDGLY  
ALMSRCWELNPQDRPSFTELREDLENTLKALPPAQEPDEIYVNMDEGGGYPEPPGAAGGADPPTQPDPK  
DSCSCLTAAEVHPAGRYVLCPSAQPADRGSPAAGQEDGA

Tubulin cofactor D

GH1-13-PCR-G3F1 (SEQ ID NO:7)

CTTCGGCAGCAGGGCTGGTTGCTCTCAGGGAGTCTGCAGCCATCGAGGCACCTGAGGACAGTGGCAGCATAGGGCA  
AACAGTCTTACGTTTCCATGTTAAATATTGTGCCAGGGCCTGCAGCGTCCCATCCATGGTGATGACCCCCCTGC  
ATGGTCTGGAAGGAGGAACGGGCCAGATTGACAGGCTCCAGGAACTCAGCCATCTGCTTGACATC  
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>gi|8400735|ref|NM\_005993.2| Homo sapiens tubulin-specific chaperone d (TBCD), mRNA (SEQ ID NO:8)

TAGCGGGCGCTCCTTCATCCCTCATCCCTCATCCCTGGCTCTAGCGGAGTGGGATCTGC  
GAACACGTGAGGCGGGGGCGCGGTCCCCCAGGCTGCCAGATGCCCTGAGCGACGAACCGGCCGGGTG  
GCCCGAGGAGGAGGCGAGGACACTGGCCTTGGCGCGCTGGAAGCGTTGGCGAGAGCGC  
GGAGACCCGGCGCTGCTGGCCCTGCCAGGTGACGGCGCGCGAGCGCAGGTGGCTG  
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TGATGAACTGTTGGACATAGTGAAGATCAGACATCTCCAGCTTCCCTGTACATCTGGCTTTAA  
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CCTCACCCAGCCTGGCAAGCACGAATGTCATAATGGACCGTATTCTCAAATAGCAGAGTCCTACTTG  
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CCCTGCTGCCAGCTGGGAGCTGGGCTGAGCTTGTGAGCGACTGGGCTGACATTCTGAAGCCGAAGGTGGC  
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TGGTCTGCCGTCTGACTCGTGGATGTTGCTGCCGTGATCCTGAAGGCGCTGACCTACGACGAGAAGCG  
GGGTGCCCTGCCAGCGTGGCACCAACGTCAGGGACGCCCTGCTACGTCGCTGTGCCCTGCCGCTGCC  
TATGAGCCTCAGGAGCTGAAGCCCTTGTGACTGCAATCTGAGTGCAGTGGTATTGCTGCCGTGTTG  
ACCGAGACATAACTGCAGAAGAGCAGCCTGCCCTCCAGGAGAATGTGGGAGACAGGGACTTT

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CCCTCATGGTATTGATATTTGACCACAGCTGACTATTTGCCGTCGGTAACAGATCCAACGTGTTCCCTG  
 GTTATAAGTGTGTTATTGCCGGTTCTGAGTACACGCAGCCAATGATAGACCACCTGGTTACCATGA  
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 TCGTCAGTTACAGGGGCTGGGAGGACAGCTCATGAGACAAGCAGTGTGTTTAATAGAAAAGTTG  
 TCACTTTCAAAATGCCCTTAGAGGTGACACCGTAATTGATGGTTGGCAATGGCTGATAATGACACTT  
 TGAGACATCTCCATCTCATCTCAAGTCACTCCGCCAGCAGATGAAGGATGCGAGCTCGGCCCTGGC  
 TGCTCTATGCAGTGAATATTACATGAAGGAGCCGGGAGGCAGATCCCGCAATTCAAGGAGGAGCTGATC  
 ACGCAGTACCTGGCTGAGCTCGAACCCCGAGGAGATGACTCGCTGTTCTCGTGGCCTTGGCCTGGCG  
 CCCTCCAGGCTTCTCTGAAAGGCCGGCTCCAGCAGGTTCTCACAGGTTAACAGCAGTTACCCACAC  
 TTCCCCCGAGGACGTAAGTTGCTGAGTCCAGGAGAGACGGCTGAAGGCCATTGCGAGGAGTTGCCAG  
 ACTGTTGGTGTGAAAGCAGGAGCCCGAGCAAAGCTGTGCGGGAGAGAATGTTCCAGATTACTGTG  
 CGCTGCTGGGCTGCATGGACACTACACCACGGACAGCAGAGGGGACGTGGCACCTGGTCCGCAAGGC  
 CGCCATGACCAGTCTGATGGATCTGACACTCTGCTGGCTCGAGCCAGCTGAGCTGATCGAGGCCAT  
 ACCTGTGAGCGCATCATGTGCTGTGGCCAGCAGGCCAGTGAGAAGATTGACCCTTCCGTGCTCACG  
 CCGCCAGCGTGTCTGACGCTCTGCACTTGACAGCCCTCCATCCCCACGTGCCCCACCGAGGAGA  
 ACTGGAAAAGCTGTTTCCAGGTCGATGTGGCCTCCGTGAACGGAGTGCACCTCCAGGCCTCCCA  
 CGCATACCCAGCTCCTGGGCTGCCACCTACCGCTACCACGCTCTGCTGGGCTAGTCGTGCTCCCTGG  
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 CGACCCGAGGCCCTGGGAGCTCAGCGGGACCCTCTGAGATCTTGAGGACAACCTCTGAATGAG  
 AGGGTGTCCGTGCCGCTGCTGAAGACGCTGGACCACGTGCTCACCCACGGCTGCTTCGACATCTCACCA  
 CGGAGGAGGACCACCCCTTGCTGAGTTGCTGCGCTCTGTAAGAAAGAAATCAAGAATTCAAAAGA  
 TATCCAGAAAGCTCCTGTCAGGCATCGCAGTGTCTGCGGATGGTCAGTCCCGGAGCTGAGGAG  
 CAGGCCCTCTGAGCTGTGCTGCTCTGCCACGTTCCCGCTGATCCGAAGACCACGGCAGCC  
 AGGTGTACGAGACATTGTCACCTACAGTGACGCTGGGGCGGATGTGCTGGACGAGGTGGTACTGT  
 GCTCAGTGACACTGCGTGGGACCGGGAGCTGCACTGGTGGAGAGAGCAGCAGCAACCGCTGTGACCTT  
 CTGGGCGTACCCAGGCCAGCTGGTGGCCAGCCTGGTGCCTGTAAGCCAGTCCTGGAGGCCATACC  
 TCACCCCTGCTGGTGGAGGATGTTCTGAGGGAGGCCGGTGTGAAAGCCTTGACAGCTTCTGCACAGTGGTGC  
 TCCAGCTGTTGAAAGGGTAGCGCTGGCCCTGGAGGCTGGCACTAGCTGACAGCTTCTGCACCT  
 GCGCTCTGGTACTGGGTTGGACGCCCTGCTGCCTCACTGAACACAAATGTGCTTCTATAAAATCATG  
 TACCAAG

>gi|8400736|ref|NP\_005984.2| beta-tubulin cofactor D [Homo sapiens] (SEQ ID NO: 9)

MALSDEPAAGGPEEEAEDET LAFGAALEAFGE SAETR ALLGRLRE VHGGGAEREVALERFRVIMDKYQEQ  
 PHLLDPHLEWMNLLL DIVQDQTSPASLVHL AFKFLYIITKVRGYKTFLRF PHEVADVEPVLDLVTION  
 PKDHEAWTRYM LLLWLSVTCLIPFDFSR LDGNLLT QPGQARMSIMDRILQIAESYLI VSDKARDAAAVL  
 VSRFIRPDVKQSKMAEFLDW SLCNLARSSQTMQGVITMDGTQLAQIFKHGKREDCLPYAATVLRCL  
 DGCR LPESN QTLLRKLGKV LQRLGLTFLKP KVA AWRYQRGCRSLAANQLLTQGQSEQKPLILTEDDE  
 DDDVPEGVERVIEQ LLLVGLKD TVRVWSAKGIGR MAGRLP RALADDVVG SVLDCFSQETDKA WHGGC  
 LALAE LGRG LLLPSRLVDVVA VILK ALTYDEKRGACSV GTNVR DAAC YVCCAFARAYEPQELKPFVTAI  
 SSALVIAAVFD RDINCRRAA SAAFQEN VGRQGT FPHGID ILTTADYFAVGNRSNCFLVISVFIAGFPEYT  
 QPMIDHLVTMKISHWDGVIRELAARALHNLAQQA PEFSATQVFPRLLSMTLSPDLHMRHGSILACAEVAY  
 ALYKLAAQENRPVTDHLD EQAVQGLKQIHQQLYDRQLYRGLGGQLMRQAVCVLIEKLSLSKMPFRGDTVI  
 DGWQWLINDTLRHLH LISSH SRQKM DAAV SALA ALCESE YYMKEPGEADPAI QEE LITQYLAELRNPEEM  
 TRCGFSLAL GALPGFLLKGR LQQVLTGLRAVTH TSPEDV SFAESRRDGLKAIARICQTVGVKAGAPDEAV  
 CGENVSQIYC ALLGCM DDYTTDSRGDV GTW VRKAAMTSLMDL TLLLARSQPELIEAHT CERIMCCVAQQA  
 SEKIDR FRAHAASVFTL LHFDSSPPIPHVPHRGE LEKLF PRSDV ASV NWSAPS QAFPRITQ LLG LPTYRY  
 HVLLGLV SVSLGG LTESTIRH STQSL FEYMKG I QSDPQ ALGS FSGT LLQI FEDNLL NERV SVPLL KLDHV  
 LTHGCFDIFTTEEDHPFAV KLLALCKKEIKNSKDIQKL LSGIAVFCGMVQFP GDV RRQ ALLQLCLLCHR

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FPLIRKTTASQVYETLLTYSVVGADVLDEVTVLSDTAWDAELAVVREQRNRLCDLLGVPRPQLVPQPG  
AC

## Transglutaminase 2

GH1-173-PCR-G3F1 (SEQ ID NO:10)

CCAGTGTGCTTGGGTTCTCGGGCACCCCTGGATCTCCCCAAACTCATTGCGGAAGTACTCGATGAGAAGGTTGCTGTT  
CTGGTCATGGGCCGAGTTGTAGTTGGTCACGCGGGTAGGGATGCCAGGCACCTCAGCACTGTGCAGGCCACGG  
CGGCAAGACCCAGCACTGGCCATACTTGACCGCTGGCAGCCGGTTCTCCAGCGCCGAGGATGTCCACGCTGC  
CGATCCAGGACATGGGCTGACCCGAGACCCAGCACAGTGGTTAGATGATAAAGCGGCCGCTGACTAGTCTGAGG  
TCTGATACTCACTGACTGTCGTA

gi|20141877|sp|P21980|TGM2\_HUMAN Protein-glutamine gamma-glutamyltransferase  
(Tissue transglutaminase) (TGase C) (TG(C)) (Tranglutaminase 2)  
(TGase-H) (SEQ ID NO:11)

MAEELVLERCDLELETNGRDHHTADLCREKLVVRRQPFWLTLHFEGRNYEASVDSLTSVVTGPAPSQE  
AGTKARFPLRDAVEEGDWTATVVDQQDCTLSQLTTPANAPIGLYRLSLEASTGYQGSSFVLGHFILLFN  
AWCPADAVYLDSEEREQEYVLTQQGFIYQGSAKFIKNIPWNFGQFEDGILDICLILLDVNPKFLKNAGR  
CSRRSSPVYGRVVSGMVNCNDQGVLLGRWDNNYGDGVSPMSWIGSVIDLRRWKHGCQRVKYQQCWVF  
AAVACTVLRCLGIPTRVVTNYNSAHDQNSNLLIEYFRNEFGEIQGDKSEMIWNFHCVVESWMTRPDLQPG  
YEGWQALDPQEKSEGTYCCGPVPVRRAIKEGDLSTKYDAPFVFAEVNADVDWIQQDDGSVHKSIINRSL  
IVGLKISTKSVGRDEREDITHTYKYPEGSSEEREAFTRANHLNLAEKEETGMAMRIRVGQSMNMGSDFD  
VFAHITNNNTAEYVCRLLLCARTVSYNGLPECGTYKLLNLNLEPFSEKSVPLCILYEKYRDCLTESNL  
IKVRALLVEPVINSYLLAERDLYLENPEIKIRILGEPKQKRKLVAEVSLQNPPLPVALEGCTFTVEGAGLT  
EEQKTVEIPDPVVEAGEEVKVRMDLLPLHMGLHKLVNFESDKLKAVKGFRNVIIGPA

>gi|4759227|ref|NM\_004613.1| Homo sapiens transglutaminase 2 (C polypeptide,  
protein-glutamine-gamma-glutamyltransferase) (TGM2), mRNA (SEQ ID NO:12)

AACAGGGCGTGACGCCAGTTCAAACCTGAAACAAAACCCACTCAAAGTACACCAAAATAGAACCTCCT  
TAAAGCATAAATCTCACGGAGGGTCTCGGCCAGTGGAGGCCAGGGAGACCACACGGCCGAC  
CGAGGAGCTGGCTTAGAGAGGGTGTATCTGGAGCTGGAGACCAATGGCCGAGACCACACGGCCGAC  
CTGTGCCGGAGAGCTGGTGGTGCACGGGCCAGCCTCTGGCTGACCCCTGCACTTGAGGGCCGCA  
ACTACCAGGCCAGTGTAGACAGTCTCACCTCAGTGTCTGACCCGCCAGCCCTAGCCAGGAGGCCGG  
GACCAAGGCCGTTTCAACTAAGAGATGCTGTGGAGGGTGAUTGGACAGCCACCGTGGGACCAAG  
CAAGACTGCACCCCTCGCTGCAGCTCACCAACCCGCCAACGCCACATCGGCCTGTATGCCCTCAGCC  
TGGAGGCCTTCACTGGCTACCAGGGATCCAGCTTGTGCTGGGCCACTTCATTTGCTTCAACGCCCTG  
GTGCCAGGGATGCTGTACCTGGACTCGGAAGAGGAGCGGGAGGAGTATGTCCCTACCCAGCAGGGC  
TTTATCTACCAAGGGCTGGCCAAGTTCATCAAGAACATACCTTGAATTGGCAGTTCAAGATGGGA  
TCCCTAGACATCTGCTGATCCTTCTAGATGTCAACCCCAAGTCTGAAGAACGCCGGCGTGAUTGCTC  
CCGGCGCAGCAGCCCGTCTACGTGGCCGGTGGTAGTGGCATGGTCAACTGCAACGATGACCAGGGT  
GTGCTGCTGGACGCTGGACAACAACACTACGGGACGGCTCAGCCCATGTCTGGATCGGCAGCGTGG  
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CGTGGCCTGCACAGTGTGAGGTGCCTAGGCATCCCTACCGCGCTGTGACCAACTACAACCTGGCCCAT  
GACCAGAACAGCAACCTCTCATCGAGTACTCCGCAATGAGTTGGGAGATCCAGGGTACAAGAGCG  
AGATGATCTGGAACCTCCACTGCTGGGTGGAGTCGTGGATGACCCAGGCCGACCTGCAGCCGGGTACGA  
GGGCTGGCAGGCCCTGGACCCAACGCCAGGAGAAGAGCGAAGGAACGTACTGCTGTGGCCAGTTCCA  
GTTCGTGCCATCAAGGAGGGCGACCTGAGCACCAAGTACGATGCGCCCTTGTCTTGCGGAGGTCAATG  
CCGACGTGGTAGACTGGATCCAGCAGGACATGGGTCTGTGCACAAATCCATCAACCCTTCCGATCGT  
TGGGCTGAAGATCAGCACTAAGAGCGTGGGCCAGACGAGCGGGAGGATATCACCCACACCTACAAATAC  
CCAGAGGGGTCTCAGAGGAGAGGGAGGCCCTCACAAGGGCGAACCCACCTGAACAAACTGGCCGAGAAGG  
AGGAGACAGGGATGGCATGCGGATCCGTGGGCCAGACATGAACATGGCAGTGACTTGAACGTCTT

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TGCCACATACCAACAACACCGCTGAGGAGTACGTCGCCGCCTCCTGCTCTGTGCCGCACCGTCAGC  
 TACAATGGGATCTGGGCCGAGTGTGGCACCAAGTACCTGCTAACCTAACCCCTGGAGCCTTCTCTG  
 AGAAGAGCCTTCCTCTTGATCCTATGAGAAATACCGTACTGCCTACGGAGTCCAACCTCATCAA  
 GGTGCGGCCCTCCTCGTGGAGCCAGTTATCAACAGCTACCTGCTGGCTGAGAGGGACCTACCTGGAG  
 AATCCAGAAATCAAGATCCGGATCCTTGGGAGCCAAAGCAGAAACGCAAGCTGGTGGCTGAGGTGTCCC  
 TGCAGAACCCGCTCCCTGTGGCCCTGGAAGGCTGCACCTCACTGTGGAGGGGCCGGCTGACTGAGGA  
 GCAGAACGGTGGAGATCCCAGACCCGTGGAGGAGGGAGGAAGTTAAGGTGAGAATGGACCTCGTG  
 CCGCTCCACATGGGCCCTCACAAGCTGGTGGTGAACCTCGAGAGCGACAAGCTGAAGGCTGTGAAGGGCT  
 TCCGGATGTCATCATTGGCCCCCTAAGGGACCCCTGCTCCAGCCTGCTGAGAGCCCCACCTTGAT  
 CCAAATCCTATCCAAAGCTAGTGAGCAAATATGCCCTTATTGGGCCAGACCCAGGGCAGGGTGG  
 GCAGCCTATGGGGCTCGGAAATGGAATGTGCCCTGGCCATCTCAGCCTCTGAGCCTGTGGTCC  
 CCACTACCCCCCTTGCTGTGAGGAATGCTCTGTGCCAGAACAGTGGGAGCCCTGACCTGTGACTG  
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 CCTTGGGACACCCAGAGCTGGGTGGGACAGTGTAGGCCAAGGTCCCTCACATCCCAGCAGCCAA  
 GCTTAATAGCCCTCCCCCTCAACCTCACCATTGTGAAGCACCTACTATGTGCTGGGTGCCTCCCACACTT  
 GCTGGGCTCACGGGGCTCCAACCCATTAAATCACCATGGAACTGTTGGCGCTGCTCCAGGAT  
 AAGGAGACTGAGGCTTAGAGAGAGGAGGAGCCCCCTCACACCAGTGGCCTCGTGGTATAAGCAAGGC  
 TGGGTAAATGTGAAGGCCAAGAGCAGAGCTGGGCCTCTGACTCTGAGTCCACTGCTCCATTATAACCC  
 CAGCCTGACCTGAGACTGTCGAGAGGCTGTCTGGGGCTTTATCAAAAAAAAGACTCAGCCAAGACAAGG  
 AGGTAGAGAGGGACTGGGGACTGGGAGTCAGAGCCTGGCTGGTTCAGGTCCACGTCTGGCAGCG  
 ACTGCCTCTCCTCTGGGCTTTGTTCTGTTGTCAGAGGAGTGATTGAACCTGCTCATCTCAA  
 GGATCCTCTCCACTCCATGTTGCAATACACAATTCC

>gi|4759228|ref|NP\_004604.1| transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase) [Homo sapiens] (SEQ ID NO:13)  
 MAEELVLERCDLELETNRDHHTADLCREKLVVRQPFWLTLHFEGRNYQASVDSLTSVVTGPAPSQE  
 AGTKARFPLRDAVEEGDWTATVVVDQQDCTLSQLTPANAPIGLYRLSLEASTGYQGSSFVLGHFILLFN  
 AWCPADAVYLDSSEERQEYVLTQQGFIYQGSAKFIKNIPWNFGQFDGILDICLILLDVNPKFLKNAGR  
 CSRRSSPVYGRVGSVMNCNDQGVLLGRWDNNYGDGVSPMSWIGSVIDLRRWKHGCQRVKYQQCWVF  
 AAVACTVLRLGIPTRVNTYNSAHQNSNLLIEYFRNEFGEIQGDKSEMIWFHCVVESWMTRPDQPG  
 YEGWQALDPTPQEKEGTYYCCGPVPVRAIKEGDLSTKYDAPFVFAEVNADVVDWIQQDDGSVHKSI  
 RSLIVGLKISTKSVGRDEREDITHTYKYPEGSSEEREAFTRANHLNKLAEKEETGMAMRIRVGQS  
 MNMGSDFDVFAHITNNTAEEYVCRLLLCARTVSYNGILGPECGTKYLLNLTEPFSEKSVPLCIL  
 YEKYRDCLESNIKVRAALLVEPVINSYLLAERDLYLENPEIKIRILGEPKQKRKLVAEVSLQ  
 NPLPVALEGCTFTVEGAGLT  
 EEQKTVEIPDPVEAGEEVKVRMDLVPLHMGLHKLVNFESDKLKAVKGFRNVIIGPA

>gi|13097680|gb|BC003551.1|BC003551 Homo sapiens, Similar to transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase), clone MGC:1193 IMAGE:3544757, mRNA, complete cds (SEQ ID NO:14)  
 CTCCGCCTCGGCACTGCCAGCGCCAGTGGTGCACCTGGAGGGCTCGCCGCCAGTGGAGGCCACC  
 GCCCCCGCCGACCATGGCGAGGAGCTGGTCTTAGAGAGGTGTATCTGGAGCTGGAGACCAATGGCCG  
 AGACCACACACGGCCGACCTGTGCCGGAGAACGCTGGTGTGCGACGGGGCCAGCCCTCTGGCTGACC  
 CTGCACTTTGAGGGCCCAACTACGAGGCCAGTGTAGACAGTCTACCTTCAGTGTGACCGGGCCAG  
 CCCCTAGCCAGGAGGCCGGACCAAGGCCGTTTCCACTAAGAGATGCTGTGGAGGGGTGACTGGAC  
 AGCCACCGTGGTGGACAGCAAGACTGCACCCCTCTCGCTGCAGCTCACCAACCCGGCAACGCC  
 CCCATGCCCTCAGCCTGGAGGCCTCCACTGGTACCGGGATCCAGGCTTGTGCTGGCCACTTCA  
 TTTGCTCTCAACGCCCTGGTGCCAGCGGATGCTGTGACCTGGACTCGGAAGAGGAGCAGGAGTA  
 TGTGCTCACCAGCAGGGCTTATCTACCAAGGGCTGCCAAGTCATCAAGAACATACCTGG  
 ATTTGGCAGTTGAAGATGGGATCCTAGACATCTGCTGATCCTAGATGTCAACCCCAAGT  
 CAACTGCTGAAGCAGCCGGTACTGCTCCGCCAGCAGCCCCGTACGTGGCCGGTGGT  
 GAGTGGCATGGCAAACGCCGAGCAGCCGAGCAGCCGAGCAGCCGAGCAGCCGAGCAGCCGAGCAG

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CTGCAACGATGACCAGGGTGTGCTGGGACGCTGGACAACAACACTACGGGACGGCGTCAGCCCCATG  
TCCGGATCGGCAGCGTGGACATCCTGCAGCGCTGGAAAGAACACGGCTGCCAGCGCTCAAGTATGCC  
AGTGCTGGGCTTCGCCCGTGCACAGTGTGAGGTGCTGGCATCCCTACCCGCGTCGTGAC  
CAACTACAACCTCGGCCATGACCAGAACAGAACCTCTCATCGAGTACTCCGCAATGAGTTGGGAG  
ATCCAGGGTACAAGAGCAGATGATCTGAACTTCACTGCTGGTGGAGTCGTGGATGACCAGGCCGG  
ACCTGCAGCCGGGTACGAGGGCTGGCAGGCCCTGGACCCAACGCCCAAGGAGAACAGCGAAGGGACGTA  
CTGCTGTGGCCCAGTCCAGTTCGTGCCATCAAGGAGGGCACCTGAGCACCAAGTACGATGCGCCCTT  
GTCTTGCAGGGTCAATGCCACGTGGTAGACTGGATCCAGCAGGACGATGGTCTGTGACAAATCCA  
TCAACCCTCCCTGATCGTGGGCTGAAGATCAGCACTAACAGAGCGTGGGCCAGACGAGCGGGAGGATAT  
CACCCACACCTACAAATACCCAGAGGGTCTCAGAGGGAGGGCCTCACAGGGCAACCACCTG  
AACAAACTGCCGAGAAGGAGGGACAGGGATGCCATCGGGATCCGTGTGGCCAGAGCATGAACATGG  
GCAGTACTTGCAGCTTGCCTCACCAACACCCGCTGAGGAGTACGCTGCCGCTCTGCT  
CTGTGCCCGACCCTCAGCTACAATGGGATCTGGGCCAGTGTGGCACCAAGTACCTGCTCAACCTC  
AACCTGGAGCCTTCTGGTAAAGCCCTGTGTTCTGGAGCATTGACCGCCAACGTACAACATGC  
TAGGTAGTGAACCTAAAAAAAAAAAAAAA

>gi|13097681|gb|AAH03551.1|AAH03551 Similar to transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase) [Homo sapiens] (SEQ ID NO:15)

MAEELVLERCDLELETNGRDHHTADLCREKLVRRQPFWLTLHFEGRNYEASVDSLTSVVTGPAPSQE  
AGTKARFPLRDAVEEGDWTATVVDQQDCTLSQLLTPANAPIGLYRLSLEASTGYQGSSFVLGHFILLFN  
AWCPADAVYLDSEERQEYVLTQQGFIYQGSAKFIKNIPWNFGQFEDGILDICLILLDVNPKFLKNAGR  
CSRRSSPVYVGRVVSVMNCNDQGVLLGRWDNNYGDGVSPMSWIGSVIDLRRWKHGCQRVKYQCWVF  
AAVACTVLRLGIPTRVNTYNSAHQNSNLLIEYFRNEFGEIQGDKSEMIWFHCWVESWMTRPDLOPG  
YEGWQALDPTPQEKGESTYCCGPVPVRAIKEGDLSTKYDAPFVFAEVNADVVDWIQQDDGSVHKSINRSL  
IVGLKISTKSVGRDEREDITHTYKYPEGSSEEREAFTRANHLNKLAKEETGMAMRIRVGQS  
MNMGSDFD  
VFAHITNNTAEEYVCRLLLCARTVSYNGILGPECGTKYLLNLNLEPFSKALCSWSIC

>gi|339577|gb|M98478.1|HUMTGH1A Human transglutaminase mRNA, complete cds (SEQ ID NO:16)

CAGGCAGTACGCCAGTCTAAATCTGAAACAGAACAAACTCAAAGTACACCAAAATAGAACCTCCTT  
AAAGCATAAATCTCACGGAGGGCTCGCCGCCAGTGGAAAGGAGCCACGCCCGCCGACATGCCGA  
GGAGCTGGCTTCTAGAGGGTGTGATCTGGAGCTGGAGACCAATGCCGAGACCACACGCCGACCTG  
TGCCTGGAGAGCTGGTGGTGCACGGGCCAGCCCTCTGGCTACCCCTGACTTGAAGGGCCGAACT  
ACGAGGCCAGTGTAGACAGTCTCACCTCAGTGTGACCGGCCAGCCCTAGCCAGGAGGCCGGAC  
CAAGGCCGTTTCAACTAAGAGATGCTGGAGGAGGGTACTGGACAGCCACCGTGGGACAGCAA  
GAUTGCACCCCTCGCTGAGCTCACCAACCCGCCAACGCCACCGTGTATGCCCTCAGCCTGG  
AGGCCTCACTGGCTACCAAGGGATCCAGCTTGTGCTGGGCCACCTCATTGCTCTCAACGCCGGT  
CCCAGCGATGCTGTACCTGGACTCGGAAGAGGAGCCAGGAGTATGCTCACCAGCAGGGCTT  
ATCTACCAGGGCTCGGCCAAGTTCATCAAGAACATACCTTGGAAATTGGCAGTTGAAGATGGATCC  
TAGACATCTGCTGATCCTCTAGATGTCAACCCCAAGTTCTGAAGAACGCCGGCGTACTGCTCCCG  
CCGCAGCAGCCCCGTCACGTGGCCGGGTGTGGAGTGGCATGGCAACTGCAACGATGACCAGGGTGTG  
CTGCTGGGACGCTGGACAACAACACTACGGGACGGCGTCAGCCCATGTCCTGGATCGCAGCGTGGACA  
TCCCTGCCGCGCTGGAAAGAACACGGCTGCCAGCGCTCAAGTATGCCAGTGTGGCTTCGCCCGT  
GCCCTGCACAGTGTGAGGTGCCATCCCTACCCGCGTGTGACCAACTACAACCTGCCCATGAC  
CAGAACAGCAACCTCTCATCGACTTCCGCAATGAGTTGGGAGATCCAGGGTGACAAGAGCGAGA  
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CTGGCAGGCCCTGGACCAACGCCCAAGGAGAACAGCGAAGGGACGTACTGCTGTGGCCAGTTCCAGTT  
CGTGCCTCAAGGAGGGGACCTGAGCACCAAGTACGATGCGCCCTTGTCTTGCAGGGAGGTCAATGCCG  
ACGTGGTAGACTGGATCCAGCAGGACGATGGTCTGTGACAAATCCATCAACCGTCCCTGATCGTTGG  
GCTGAAGATCAGCACTAAGAGCGTGGGCCAGACGAGCGGAGGATATCACCCACACCTACAAATACCA  
GAGGGTCCTCAGAGGAGAGGAGGCCCTCACAGGGCAACCAACTGAACAAACTGCCGAGAAGGAGG

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AGACAGGGATGCCATCGGATCCGTGTGGCCAGAGCATGAACATGGCAGTGACTTGACGTCTTGC
CCACATCACCAACAACACCGCTGAGGAGTACGTCTGCCGCTCCTGCTCTGCCGCACCGTCAGCTAC
AATGGGATCTGGGCCAGTGTGGCACCAAGTACCTGCTAACCTAACCTGGAGCCTTCTGGTA
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>gi|339578|gb|AAA36739.1| transglutaminase (SEQ ID NO:17)  
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AGTKARFPLRDAVEEGDWTATVVDQQDCTLQLTTPANAPIGLYRLSLEASTGYQGSSFVLGHFILLFN  
AWCPADAVYLDSEEERQEYVLTQQGFIYQGSAKFIKNIWNFGQFEDGILDICLILDVNPKFLKNAGR  
CSRSPVYVGRVWSGMVNNDQGVLLRWDNNGDGVPMSWIGSVDLRRWKNHGCQRVKYGQCWVF  
AAVACTVLRLCGIPTRVVNTNNSAHDQNSNLIEYFRNEFGEIQGDKSEMIWFHCVESWMTRPDQPG  
YEGWQALDPTPQEKGSEGTYCCGPVVRAlKEGLDLSTKYDAPFVFAEVNADVWDWIQQDDGSVHKSI  
IVGLKISTKSVGRDEREDITHTYKYPEGSSEEREAFTRANHLNLAKEETGMAMRIRVGQSMNMGSDFD  
VFAHITNNTAEEYCRLLLARTVSYNGILGPECGTKYLLNLNLEPSKGALCSWSIC

Cytosine deaminase

GH1-27-PCR-G3F1 (SEQ ID NO:18)  
CCAGCGGTGGCTCCAGTGTGTGGCTCGGGACGTGTGCCATGCCAGCTGAATGCCATCATGAACAAAAATTGAC  
CGATGTGAAAGGCTGTAGTATGTATGTTGCCCTGTTAATGAATGCGCTAACGCTCATCCAGGCAGGTA  
TAAAAGAAGTGTATTTCTTGTGTTGATAAAATACCATGATAGTGACGAGGCAACTGCTGGAGGCTCTGTTAATAT  
GGCGGGGTGACATTCCGAAATTCAACCGAAGTGCAGCAAGATTGTCATTGACTTTGATTCAATTAACAGCAGAC  
CGAGTCAAAGCTTCAGTGAGTTACATCTCATTCAATCTCCAGAAGATTGGGATTATCGTCTCTAAGAGGTTGCTA  
ATGCCCTTCATCTGAAGTTACACATAACTCTTACTAGCCAGTATGCCAAAAGTAGGCATCTTAAGAATATAAGC  
CTCCAATCTCCTTACTGTCTCTGTACATGGAATCTACATGTGTTGAACTATTGCTTTAGGGATTAAAATA  
GGGGAGCCTGGTGGCCTGGTGACAGGGGCTAGAACGAGAGTGCCTCCCTCTGTGTCCTGGCTGGCTGGGAT  
GCTGTGGCTCTCAGAGGAGCATCAGCCTGTCTGTCATCTGCTGGATCCGGCAG

>gi|23503055|sp|P32321|DCTD\_HUMAN Deoxycytidylate deaminase (dCMP deaminase) (SEQ ID NO:19)  
MSEVSKKKRDDYLEWPEYFMAVAFLSAQRSKDPNSQVGACIVNSENKIVGIGYNGMPNGCSDDVLPWRRT  
AENKLDTKYPVCHAEINAIMMNKNSTDVKGCSMYVALFPCNECAKLIQAGIKEVIFMSDKYHDSDEATA  
ARLLFNMAGVTFRKFIPKCSKIVIDFDSINSRPSQKLQ

>gi|4503276|ref|NM\_001921.1| Homo sapiens dCMP deaminase (DCTD), mRNA (SEQ ID NO:20)  
ATGAGTGAAGTTCTGCAAGAAACGGGACACTATTGGAATGCCAGAGTATTTATGGCTGGCCT  
TCTTATCAGCACAGAGAAAGCAAAGATCCAAATTCCCAGGTGCGCCCTGCATCGTAATTCAAGAAA  
GATTGTCGGGATTGGGTACAATGGGATGCCAAATGGGTGAGTGTGACGTGTTGCCCTGGAGAAGGACA  
GCAGAGAATAAGCTGGACACCAAATACCGTACGTGTCCATGCCAGCTGAATGCCATCATGAACAAA  
ATTGACCGATGTGAAAGGCTGTAGTATGTATGTCGCCCTGTTCCCTGTTAATGAATGCGCTAACGCTCAT  
CATCCAGGCAGGTATAAAAGAAGTGTATTTACGTCTGATAAAATACCATGATAGTGACGAGGCAACTGCT  
GCGAGGCTCTGTTAATATGCCGGGTGACATTCCGAAATTACCGAAGTGCAGCAAGATTGTCA  
TTGACTTGATTCAATTAAACAGCAGACCGAGTCAGTCAGTGAGTTACATCTCATTCAATCTCCAG  
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CACAGGGCTAGAACGAGAGTGCCTCCCTCTGTGTCCTGGCTGGATGCTGGTGGCTCTCAGA  
GGAGCATCAGCTGTCTGTCATCTGCTGCGATCCGGCAGCCTCTTCACTGCTACATGTGCTGGAGGAC  
AAATAAATAATTGTGGTTGTTCTTAATGGGACGAGCAGACACTGATGAACATCTGCCCAAGT

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GAAGCATGGCATATACTGCCCTTGAAGAAAATTAGGCCTAAATGACAGTAGCATTGAAGTGTTGCTG  
 CAGAGTTGAGGGAAACCCCCAGCCACCCTCCCGAATCCGAGATAGGGTGGCACATCTGTCTGACAGAC  
 GAGGAGTGTAACTGAACCAGGAATATTCCTCCATTCTGCTCTCCACTGCACACAGGGTGGCACA  
 TTATCCCTCTGGGGGTGGGACCCCTGTTGGCTCAATTGGTTGGTACATGGAGCTCT  
 TCCATTCTGTTAGCTGAATAATGAGTTGTTCTAGAGGAGACAGCCTGCTCTCCTTGTGCCAAA  
 GCCCATGCCCTGCCGTGGCAGCTGGGGTGTGGATGGGAGGGTCCCCAACATGGATGTGTTGCC  
 TCCTCCGCATGCCAACCGCAGTTCATGTACAAGGCCCTGCAACTGGAGAGAAAATTAACTCCTATCCC  
 GTGAGTGGATTGTGAGAAAATTCCACCCACGTGGAGACAGCTACTGCAGCACTGTTGGTGTGAGCTC  
 TTCTGTGCCCTGGCTCCATGCTTCACCTACACAAGCATCACCTCCTAATACCGCGGGCGGGAGCG  
 TGTTGGCTGTGCCCTCTCTTAATCTCATTTAATTAAACATGCTCAGTACCTGTGTTGAGAAA  
 AGGCTTTCTTATCTAAAGATTATTACCTTTAAAGTGTCTTATTTCATGAGTTTTATTGT  
 CTCTGAGATTGTATTCCACATTCTAGGGTATTCTGTAATTGGCTCCTAACCATATTAAAATCT  
 TATTAATCT

>gi|4503277|ref|NP\_001912.1| dCMP deaminase [Homo sapiens] (SEQ ID NO:21)  
 MSEVSKRDDRLEWPEYFMAVAFLSAQRSKDPNSQVGACIVNSENKIVGIGYNGMPNGCSDDVLPWRRT  
 AENKLDTKYPVCHAEINAMKNSTDVKGCSMYVALFPCNECAKLIQAGIKEVIFTSKYHDSDEATA  
 ARLLFNMAGVTFRKFIPKCSKIVIDFDSINSRPSQLQ

Peptidase M41 (Paraplegin)

GH1-40-PCR-G3F1 (SEQ ID NO:22)

GTGGAAATGCCCTGTTACTCTGTGGGATGACGGCAGTGGGCCTGCCATCCTGTGGTATGTTCCGTCTGCCGG  
 GATGACTGGAAGGGAAAGGTGGATTCACTGCTTTAATCAGCTAAAATGGCTCGTTCACCATGTGGATTGGAAGA  
 TGGGAAAGGGAGTCAGCTCAAAGACGTGGCAGGAATGCACGAAGCCAACCTGGAAAGTCCGAGTTGTGGATTA  
 TCTGAAGAGGCCAGAACGCTCCCTCAGCTGGCGCCAGGTCCAAAGGGCGCACTGCTGCTCGGCCCCCGGCTG  
 TGGGAAGACGCTTCTGCCAAGGGCGTGGCACGGAGGCTCAGGTGCCCTCTGGCATGCCGGCCAGAGTCGT  
 GGAGGTATGGAGGCCCTGGCGTCCCGTGTGGAGGCTCTTAAGGAAGGCCAGGCCGGCCCTGCATCGT  
 CTACATCGATAGATCGACGGTGGCAAGAACGCTCCACCACCATGTCGGCTCTCCAACACNGAGGAGGAGCA  
 GACGCTAACCAAGCTCTGGTNAAGAAATGGATGAAATGGGTACACAGACCATGTCATGTCCTGGCGTCCACGAA  
 ACCGAGCTGACATTGGACGGTGTCTTATAGGCCAGGCCAACGGGACGTCTTTGATCT

>gi|4507172|ref|NM\_003119.1| Homo sapiens spastic paraplegia 7, paraplegin (pure and complicated autosomal recessive) (SPG7), mRNA (SEQ ID NO:23)

TTTCAGGCCAACATGGCGTGTGCTGCTGCTCCGTGCCCTCCGCCGGGTCAGGCCCGGGCTC  
 GGCGCTGTGGGCCAGGCCGCTGGAGTCCAGGGTCCCCGCCAGGCCGGAGGGGGCGGGCGTA  
 CATGGCCAGGCCCTCCGGGGACCTCGCCGAGGCTGGAGGCCAGCTGCAAGAGCTTACAATTGAGA  
 CTGCTAACCCCTACCTTGAAAGGATCAACGGATTGTTGAAACACATTAGTTGAGAACATCCAGTCA  
 GACTCTGGCAACTTTAGGTGGTACTTTCTATTAAACACCTCAAGGTTGAAAGCAGAAGAATAAGGAGAA  
 GGATAAGTCAAAGGGAAAGGCCTGAAGAGGACGAAGAGGAGAGGAGACGCCGTGAGCGGGACGACAG  
 ATGTACCGAGAGCGGCTGCGCACCTGCTGTCATCGGGTTGTCATGAGCTCTGAATGCTCTCAGCA  
 CCAGCGGAGGCAGATTCTGGAACGACTTGTCACGAGATGCTGGCAAGGGAGGGTGCAGCGCGT  
 CCAGGTGGTGCCTGAGAGCGACGTGGGAAGTCTACCTGCACCTGGAGCCGTGGTGTGTTGGCCGCT  
 CGGCTAGCCTTGATGTACCGAATGCAGGTTGCAAATATTGACAAGTTGAAGAGAAGCTCGAGCAGCTG  
 AAGATGAGCTGAATATCGAGGCCAAGGACAGGATCCCAGTTCTACAAGCGAACAGGATTCTTGAAA  
 TGCCCTGTAAGTGTGGGATGACGGCAGTGGCCTGCCATCCTGTGGTATGTTCCGTCTGCCGG  
 ATGACTGGAAGGGAAAGGTGGATTCACTGCTTTAATCAGCTAAAATGGCTCGTTCACCATGTGGATG  
 GGAAGATGGGAAAGGAGTCAGCTCAAAGACGTGGCAGGAATGCACGAAGCCAACCTGGAAAGTCCGCGA  
 GTTGTGGATTATCTGAAGAGGCCAGAACGCTTCCAGCTTGGCGCCAAGGTCCAAAGGGCGCACTG  
 CTGCTCGGCCCGGGCTGTGGGAAGACGCTGCTGGCCAAGGGCTGGCACGGAGGCTCAGGTGCC  
 TCTGGCGATGGCGGGCCAGAGTTGTCAGTGGAGGCTCATTGGAGGCTCGGCGTGGCGGAGCCT  
 CTTAAGGAAGGCCAGGCCGGCCCTGCATCGTACATCGATGAGATCGACGCGGTGGCAAGAAG

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CGCTCCACCACCATGTCCGGCTTCTCCAACACGGAGGAGGAGCAGACGCTCAACCAGCTTCTGGTAGAAA  
TGGATGGAATGGGTACCACAGACCATGTCATCGTCCTGGCGTCCACGAACCGAGCTGACATTGACGG  
TGCTCTGATGAGGCCAGGCCACTGGACCGCACGTCTCATTGATCTCCCACGCTGCAGGAGAGGCCG  
GAGATTTGAGCAGCACCTGAAGAGCCTGAAGCTGACCCAGTCAGCACCTTACTCCCAGCCTG  
CAGAGCTGACACCAGGATTCACTGGGCTGACATGCCAACATCTGCAATGAGGCTGCCGTGACGCC  
GCCGGAGGGACACACTCCGTGACACTCTCAACTTCGAGTACGCCGTGGAGCGCCTCGCAGGGACT  
GCCAAAAAGAGCAAGATCCTGTCCAAGGAAGAACAGAAAGTGGTGCCTTCATGAGTCGGGCCACGCCT  
TGGTGGGCTGGATGCTGGAGCACACGGAGGCCGTGATGAAGGTCTCCATAACCCCTCGGACAACGCC  
CCTGGGCTTGCTCAGATGCTCCCCAGAGACCAGCACCTTCAACAGAGGTCACTTCTGGGCACAGGACG  
TGCATGGCCTTGGGAGGACGGGCTCGGAAGCAGTCCTTCAACGAGGTCACTTCTGGGCACAGGACG  
ACCTGAGGAAGGTCAACCGCATGCCACTCCATGGTGAAGCAGTTGGGATGGCACCTGGCATGGGCC  
CATCTCCTTCCCTGAGGCCAGGAGGGCTCATGGCATGGGCCACTGGGAGGCCAGGCC  
CAGATGATGGACCATGAAGCAAGACTGCTGGCAAGGCCACTAGACACACCCGAGAAGGTGCTGCAGG  
ACAACCTGGACAAGTTGCAGGCCTGGCAAACGCCCTCTGGAAAAGGAAGTGATAAAACTATGAGGACAT  
TGAGGCTCTCATGGCCGCCGCCCCATGGCGAAGAAATGATGCAACCGCAGAGGTGGATGACGCC  
CAGAGGGAGAACAGGACTTGGCGAGGAGGAGACCGAAGAGACCCAGCAGCCTCCACTGGAGGCGAAG  
AGCCGACTTGGCCAAGTAGTTGGAGGTGTTGCTGACGTGCGGGTGGTCCGGGAAGTGAGGGCTCAC  
TCAGCCACCTGAGTTGCTTTCACTGAGGTTGCACTTCTCTCGCGGCCCTCAGTAGTCCCTGCACA  
GTGACTTCTGAGATCTGTTGATTGATGACCCATTGATGATTAAAGTTCTCTGCAGAAAACACTGACG  
GAGTCTGTGTTGAGTCGTTCCCTATGGGAAGGTTATCAGTGCCTCCGAGTGAGCATGGAACA  
CTTCGAGTTCCCAGGGTTATAGACAGTCGTTCCAGTGTGGCTGAGGCCACCCAGAGGCAGCAGACATT  
CAGACTCCAAACAGACCCCTGTTCATGCCGACGCTGACGCCAGGCCAGTTCTGTGGCTCCCTCGGA  
ATGCTAAGGGGATCGGACATGAAAGGACCCCTGTGAGCCATTGCTTATCTCAGCGGCCCTGTATCCA  
GCTCACTCATCAATGGGCCAGTCAGGCCAGGACTCACCAGTCCCTGCTGCTGAGTGTGGGATGCC  
CCATGTGGACTGGTGCAGTTGAGGACTTCTGCTGGCTAGTCACGCATGCAGTGTGGGATGCC  
GTTTTACTGCTCTGAGAATTGTTGAGATACTTACTAATAAACTGTGTAGTTGGAAAAAAAAAAAA  
AAAAAA

>gi|4507173|ref|NP\_003110.1| paraplegin [Homo sapiens] (SEQ ID NO:24)  
MAVLLLLLRALRRGPGRPRLWPGPAWSPGFPARPGRGRPYMASRPPGDLAEAGGRALQLQLLLTP  
TFEGINGLLKQHLVQNPVRLWQLLGGTFYFNTSRLKQKNKEDKSKGKAPEEDEERRRERDDQMYRE  
RLRTLIVAVVMSLLNALSTSGGSISWNDFVHEMLAKGEQRVQVVPESDVVEVYLHPGAVVFGPRLAL  
MYRMQVANIDKFEEKLRAEDELNIEAKDRIPVSYKRTGFFGNALYSVGMATAVGLAIWYVFRLAGMTGR  
EGGFSAFNQLKMARFTIVDGKMGKVSKFDVAGMHEAKLEVREFVDYLKSPERFLQLGAKVPKGALLGP  
PGCGKTLLAKAVATEAQVPLAMAGPEFVEIGGLGAARVSLFKEARARAPCIVYIDEIDAVGKCRSTT  
MSGFSNTEEEQTLNQLVEMDMGTTDHVIVLASTNRADILDGALMRPGRQLDRHVFIDLPTLQERREIFE  
QHLKSLKLTSSTFYSQR LAELTPFGSGADIANICNEAALHAAREGHTSVHNLFEYAVERVLAGTAKKS  
KILSKEEQKVVAFHESGHALVGWMLHETEAVMKVSI PRTNAALGFAQMLPRDQHLFTKEQLFERMCMAL  
GGRASEALS FNEVTSGAQDDLRLKVTRIAYSMVKQFGMAPGIGPISFPEAQEGLMGIGRRPFSQGLQQMD  
HEARLLVAKAYRHTEKVLDQNLDKLQALANALLEKEVINYEDIEALIGPPP HGPKKMIAPQRWI DAQREK  
QDLGEETEETQQPPLGGEETPTWPK

CD13 Aminopeptidase

GH1-72-PCR-G3F1 (SEQ ID NO:25)  
AGGCCAGGCCTAGGGGGGTTGGCATGAGCGGGCAGCGCGTGGAGGTGCTCAGGCAGCCTGGGTATCAGGAAC  
TAGACTGGCTCACAGGCAGAGAGAACGAGCTGGGCTGGAGACTTTGTCCTTGAGGGAGGACACTGGTGCCTCGGGCTCC  
AGGAATGGAGGCCCTGACCAGCCGCTGGGATGGACACATGTGGCAGCCTTGCATGGGGCCGGGTGACTTCAAGGG  
CTGGGGACTATTGCTGTTCTGTGAACCAGTGGAGCACCACCTCCTGTTCTCCTCACCCACTTATGTTGCTTT  
CGTCTTCTCCAGGGGCTTGCTCCAGGGCCGGGTGCCTAGCCGAAGCCTGTTCCCTCGTTCC

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>gi|113743|sp|P15144|AMPN\_HUMAN Aminopeptidase N (Microsomal aminopeptidase) (GP150) (Myeloid plasma membrane glycoprotein CD13) (SEQ ID NO:26)  
MAKGFYISKSLGILGILLGVAAVCTIIALSVVYSQEKENKNANSSPVASTTPSASATTNPASATTLDQSKA  
WNRYRLPNTLKPD SYQVTLR PYLTPNDR GLYVFKGSSTVRFTKEATDVI IHSKKLYTLSQGH RVVLR  
GVGGSQPPDIDKTELVEPT EYL VVHLKG SLVKDSQ YEMDSEFEGELADDLAGFYRSEYMEGNVRKV VATT  
QM QAADARKSFPCFDEPAMKA EFNITLIH PKDL TALS NMLPKGP STPL PEPDNWNVTE FHTTPKMSTYLL  
AFIVSEFDYVEKQASNGVLIRIWARPSAIAAGHDYALNVTPILNFFAGHYDTPYPLPKSDQIGLPDFN  
AGAMENWGLVTYRENSLLFDPLSSSSNKERVVTVIAHELAHQWFGNLVTIEWWNDLWLNEGFASTYVEYL  
GADYAEPTWNLKDLMVLDVYRVMAVDALASSHPLSTPASEINTPAQISELFDAISYSKGASVRLMLSSF  
LSEDVFQQLASYLHTFAYQNTIYLNLDHLOEAVNNRSIQLPTTERDIMNRWTLQMGFPVITVDTSTGT  
LSQEHFL DPDNSVTRPSEFNYWIVPITSIRDGRQQDYWLMDVRAQNDLFSTSGNEVLLNLNVTGYY  
RVNYDEENWRKIQTQLQRDHSAIPVINRAQIINDAFNLASAHKVPTLALNNTLFLIERQYMPWEAALS  
SLSYFKLMFDRSEVYGPMKNYLKQVTPLFIHFRNNNTNWREI PENLMDQYSEVNAISTAC SNGVPECEE  
MVSGLFKQWMENPNNNPIHPNLRSTVYCNIAQGGE EWDFAWEQFRNATLVNEADKLRAALACSKELWI  
LNRYLSYTLPD LIRKQDATSTIISITNNVIGQGLVWDFVQSNWKP FNDYGGGSFSFSNL IQAVTRRFS  
TEYELQQLEQFKKDNEETFGSGTRALEQALEKT KANIKWVKENKEVVLQWFTEN SK

>gi|4502094|ref|NM\_001150.1| Homo sapiens alanyl (membrane) aminopeptidase (aminopeptidase N, aminopeptidase M, microsomal aminopeptidase, CD13, p150) (ANPEP), mRNA (SEQ ID NO:27)  
TAATTTTGC CAGTC GCT GTG GGG CT CCT CCC TT GGG GATA TAAGCCGGCTGGGCTGCT  
CCGTTCTCGCCTGGCCTGAGGCTCCCTGAGCCGCTCCCCACC ATCACCATGCCAAGGGCTTCTATAT  
TTCCAAGTCCCTGGGATCCTCTGGGATCCTCTGGCGTGGCAGCGTGTGCACAATCATCGCACTGTCA  
GTGGTGTACTCCCAGGAGAACAGAACAGCCAAACAGCTCCCCGTGGCTCCACCACCCCGTCCGCT  
CAGCCACCACCAACCCGCTGCCACCACCTGGACCAAAGTAAAGCGTGAATCGTTACCGCTCC  
CAACACGCTGAAACCCGATT CCTACCGAGTGACGCTGAGACCGTACCTCACCCCAATGACAGGGCCTG  
TACGTTTTAAGGGCTCCAGCACCGTCCGTTCACCTGCAAGGAGGCCACTGACGTCACTCATCCACA  
GCAAGAAGCTCAACTACCCCTCAGCCAGGGCACAGGGTGGCTGCGTGGTGTGGAGGCTCCAGCC  
CCCCGACATTGACAAGACTGAGCTGGAGCCACCGAGTACCTGGTGGTGCACCTCAAGGGCTCCCTG  
GTGAAGGACAGCAGTATGAGATGGACAGCGAGTTGAGGGGAGTTGGCAGATGACCTGGCGGGCTCT  
ACCGCAGCGAGTACATGGAGGGCAATGTCAGAAAGGTGGCCACTACACAGATGCAAGGCTGCA GATGC  
CCGGAAAGTCTTCCATGCTCGATGAGCCGCCATGAAGGCCAGTTCAACATCACGCTTATCCACCC  
AAGGACCTGACAGCCCTGCTCAACATGCTTCCAAAGGTCCAGCACCCACTCCAGAAGACCCA ACT  
GGAATGTCACTGAGTCCACACCACGCCAAGATGTCACGTACTTGCTGGCTTCATGTCAGTGAGTT  
CGACTACGTGGAGAACAGGCATCCAATGGTGTCTGATCCGGATCTGGGCCGGCCAGTGCCATTGCG  
GCGGGCCACGGCGATTATGCCCTGAACGTGACGGGCCCCATCCTTAACCTCTTGCTGGTCAATTGACA  
CACCCCTACCCACTCCCCAAATCAGACCA GAGATTGGCCTGCCAGACTTCAACGCCGGCGCCATGGAGAAC TG  
GGGACTGGT GACCTACCGGGAGAAC TCCCTGCTGTTGAGCCCCCTGCTCCTCCAGCAGCAACAGGAG  
CGGGTGGTCACTGTGATTGCTCATGAGCTGGCCACCA GAGTGGTCCGGAACCTGGT GACC ATAGAGTGGT  
GGAATGACCTGTGGCTGAACGAGGGCTTCGCCCTCACGTGGAGTACCTGGT GCTGACTATGCGGAGCC  
CACCTGGAACTTGAAAGACCTCATGGTGCTGAATGATGTGAGCCGTGATGGCAGTGAGTGC ACTGGCC  
TCCTCCCACCGCTGTCACACCCGCCCTGGAGATCAACAGCCGGCCAGATCAGTGAGCTGTTGACG  
CCATCTCCTACAGCAAGGGCGCCTCAGTCCTCAGGATGCTCTCCAGCTCCCTGTCAGGACGTATTCAA  
GCAGGGCCCTGGCGTCCACCTCCACACCTTGCCTACAGAACACCATCTACCTGAACCTGTGGGACCAC  
CTGCAGGAGGCTGTGAACA ACCGGTCCATCCA ACTCCCCACCACCGTGC GGAGCATCATGAACCGCTGGA  
CCCTGCAGATGGGCTTCCCGGT CATCACGGTGGATACCAGCACGGGGACCC TTTCCCAAGGAGC ACTT CCT  
CCTTGACCCGATTCCAATGTTACCCGCCCTCAGAATTCAACTACGTGTGATTGTGCCCATCACATCC  
ATCAGAGATGGCAGACAGCAGCAGGACTACTGGCTGATAGATGTAAGAGCCCAGAACGATCTCTCAGCA  
CATCAGGCAATGAGTGGGTCTGCTGAACCTCAATGTGACGGGCTATTACGGGGTGA ACTACGACGAAGA  
GAAC TGGAGGAAGATT CAGACTCAGCTGCAGAGAGACCACTCGGGC ATCCCTGTCATCAATCGGGCACAG  
ATCATTAAATGACGCCTCAACCTGGCCAGTGCCCATAAGGTCCCTGTCACTCTGGCGCTGAACAAACACCC  
TCTTCCCTGATTGAAGAGAGACAGTACATGCCCTGGGAGGCCCTGAGCAGCCTGAGCTACTTCAAGCT

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CATGTTGACCGCTCCGAGGTCTATGGCCCCATGAAGAACTACCTGAAGAACGCAGGTACACACCCCTCTTC  
ATTCACTTCAGAATAATACCAACAACGGAGATCCCAGAAAACCTGATGGACCAGTACAGCGAGG  
TTAATGCCATCAGCACCGCCTGCTCCAACGGAGTTCCAGAGTGTGAGGAGATGGTCTCTGGCCTTTCAA  
GCAGTGGATGGAGAACCCAATAATAACCCGATCCACCCAAACCTGCGGTCCACCGTCTACTGCAACGCT  
ATCGCCCAGGGCGGGAGGAGTGGGACTTCGCGCTGGGAGCAGTCCGAAATGCCACACTGGTCAATG  
AGGCTGACAAGCTCAGGGCAGCCCTGGCCTGCAGCAAAGAGTTGAGCTCTGAACAGGTACCTGAGCTA  
CACCCCTGAACCCGGACTTAATCCGGAAGCAGGACGCCACCTTACCATCATCAGCATTACCAACAACGTC  
ATTGGGCAAGGTCTGGTCTGGGACTTGTCCAGAGCAACTGGAAGAAGCTTTAACGATTATGGTGGTG  
GCTCGTTCTCCTCTCCAACCTCATCCAGGAGTGCACAGCACGATTCTCCACCGAGTATGAGCTGAGCA  
GCTGGAGCAGTCAAGAAGGACAACGAGGAAACAGGCTCGGCTAGGCACCCGGGCTGGAGCAAGCC  
CTGGAGAAGACGAAAGCCAACATCAAGTGGGTGAAGGAGAACAGGAGGTGGTCTCCAGTGGTACAG  
AAAACAGCAAATAGTCCCCAGCCCTGAAGTCACCCGGCCCGATGCAAGGTGCCCCACATGTGTCCATCC  
CAGCGGCTGGTGCAGGGCCTCCATTCTGGAGCCGAGGCACCAGTGTCTCCCTCAAGGACAAAGTCT  
CCAGCCCACGTTCTCTGCCTGTGAGCCAGTCTAGTCCCTGATGACCCAGGCTGCCTGAGCACCTCCCA  
GCCCTGCCCTCATGCCAACCCGCCCTAGGCCTGGCATGGCACCTGTCGCCAGTGCCCTGGGCTGA  
TCTCAGGGAGGCCAGCTCCAGGGCCAGATGAGCAGAAGCTCTCGATGGACAATGAACGGCCTGCTGG  
GGCGCCCTGTACCCCTTTCACCTTCCAAAGACCTAAATCTGAGGAATCAACAGGGCAGCAGATC  
TGTATATTTTTCTAAGAGAAAATGAAATAAAGGATTCTAGATGAAAAAAAAAAAAAA

>gi|4502095|ref|NP\_001141.1| membrane alanine aminopeptidase precursor;  
microsomal aminopeptidase; Alanyl (membrane) aminopeptidase (aminopeptidase  
N, aminopeptidase M, [Homo sapiens] (SEQ ID NO:28)  
MAKGFYISKSLGILGILLGVAAVCTIIALSVVYSQEKNKNANSSPVASTTPSASATTNPASATTLDQSKA  
WNRYRLPNTLKPDSYQVTLPYLTPTNDRGLYVFQGSSTVRFTCKEATDVIIHSKKLYTLSQGHVVLR  
GVGGSQPPDIDKTELVEPTEYLVVLKGSLVKDSQYEMDSEFEGELADDLAGFYRSEYMEGNVRKVVATT  
QMQAADARKSFPCFDEPAMKAEFNITLHPKDLTALSNMLPKGPSTPLPEDPNWNVTEFHTTPKMSTYLL  
AFIVSEFDYVEKQASNGVLIRIWARPSAIAAGHGDYALNVTPILNFFAGHYDTPYPLPKSDQIGLPDFN  
AGAMENWGLVTYRENSLLFDPLSSSSSNKERVVTVIAHELAHQWFGNLTIIEWNDLWLNEGFASTYVEYL  
GADYAEPTWNLKDLMVLNDVYRVMAVDALASSHPLSTPASEINTPAQISELFDAISYSKGASVLRMLSSF  
LSEDVFKQGLASYLHTFAYQNTIYLNLWDHLQEAVNNRSIQLPTVRDIMNRWTLQMGFPVITVDTSTGT  
LSQEHFLLDPDSNVTRPSEFNYWIVPITSIRDGRQQDYWLIDVRAQNDLFSTSGNEWVLLNLNVGTYY  
RVNYDEENWRKIQTQLQRDHSAIPVINRAQIINDAFNLASAHKVPVTLALNNTLFLIEERQYMPWEAALS  
SLSYFKLMFDRSEVYGPMKNYLKQVTPLFIHFRNNNNWREIPENLMDQYSEVNAISTACSGNGVPECEE  
MSVGLFKQWMENPNNNPIHPNLRSTVYCNAIAQGGEEDWAQEQRNATLVNEADKLRAALACSKELWI  
LNRYLSYTLPNDLIRKQDATSTIISITNNVIGQGLWDFVQSNWKKLFNDYGGGSFSFSNLIQAVTRRFS  
TEYELQQLEQFKKDNEETFGSGTRALEQALEKTKANIKWVKENKEVVLQWFTENSK

PRK-1

GH1-54-PCR-G3F1 (SEQ ID NO:29)

TCTTTCCGCCACGCACTACAGCACCCCTGGCAAGCCGCCGCTCACAGGGACCTGAGGTACGAGTGGTGGG  
CTGCAGAGACCTCCAGAGACCATCCCGTGAACCCCTACCCCTCAATGGGGGACCTGGACCCAGACAGCGCCC  
CCCTCCGTAGCCGCCAGCCGGGCCAGTAAACCCAGCACAGTGGTAGATAGATAAAGCGCCGCTGACTAG  
TCTGAGGTCTGATACTCACTGACGTGATACGT

>gi|4506072|ref|NM\_002741.1| Homo sapiens protein kinase C-like 1 (PRKCL1), mRNA (SEQ ID NO:30)

TGAGTAAATCGATACATCATCGCGCTCTGGCCGCCCTCCCTCCGACGATGGGGACCCCTGGCG  
GGCGCAGGAGGACATGGCCAGCGACGCCGTGCAGAGTGAGCCTCGCAGCTGGTCCCTGCTAGAGCAGCT  
GGCCTGGCCGGGGCAGACCTGGCGCCCCGGGTACAGCAGCAGCTGGAGCTGGAGCGGGAGCGGCTG  
CGCGGGAAATCCGCAAGGAGCTGAAGCTGAAGGAGGTGCTGAGAACCTGCGCGGGCACCACGTACC

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TGGGCCGCAGCCTGGCCCCGTAGAGCTGCTGCTGCGGGCTCCTCGCGCCGCCTGACACTGCTGCACCA  
 GCAGCTGCAGGAGCTGCACGCCAACGTGGTCTCCGACCCGGCGGCCACCCACGATGGCCCCAGTCC  
 CCTGGTGCGGGTGGCCCCACCTGCTCGGCCACCAACCTGAGCCGCGTGGCGGGCTGGAGAAGCAGTTGG  
 CCATTGAGCTGAAGGTGAAGCAGGGGGCGGAGAACATGATCCAGACCTACAGCAATGGCAGCACCAAGGA  
 CCGGAAGCTGCTGACAGCCCAGCAGATGTTGCAGGACAGTAAGACCAAGATTGACATCATCCGCATG  
 CAACTCCGCCGGCGCTGCAGGCCGACCAGCTGGAGAACCCAGGCAGCCCGGATGACACCCAAGGGAGTC  
 CTGACACTGGGGCTGTGGAGCTGCGCATCGAAGAGCTGCGGCACCACCTCCGAGTGGAGCACGCGGTGGC  
 CGAGGGTGCCAAGAACGTAAGTACTGCGCCTGCTAGCGCTGCCAGGGCCGGACCGCAAGGCAGTCAGCGAG  
 GCCCAGGAGAAATTGACAGAACCTAACAGAACAGCTGGGGCTGTCGGAGAACAGCTGCGGGCTCTGGAGCGAGACTTG  
 GGGAGCTGCCCGCCGACCACCCCAAGGGGGCGGCTGTCGGAGAACAGCTGCGGGCTCTCCGCTGC  
 CTTCAGCACCCGCCTGCCGGGCCCTTCCGCCACGCACTACAGCACCCCTGTCGAAGGCCGCGCCGCTC  
 ACAGGGACCTGGAGGTACGAGTGGTGGGCTGCAGAGACCTCCAGAGACCATCCGTGGAACCCCTACCC  
 CCTCAATGGGGGACCTGGGACCCCAAGACAGCCGCCCTTCCGCCACGCACTACAGCACCCCTGTCATTGAGAGGATTCCTA  
 CAGCCGAAGCGGAAGCCTCAGTGGCCGGAGCAGCCTCAAAGCAGAACAGCCGAGAACACCAGTGAAGTCAGC  
 ACTGTGCTTAAGCTGGATAACACAGTGGTGGGGCAGACGTCTTGGAGGCCATGTGGCCCCAATGCCTGGG  
 ACCAGAGCTTCACTCTGGAGCTGAAAGGGCACGGGAACGGAGTTGGCTGTGTTCTGGGGGACCGAGCG  
 GGGCCTGTGCCCCCAAATTCTGAAGTTGGAGGATTCTGGACAATGAGAGGCATGAGGTGAGCTG  
 GACATGGAACCCCAGGGCTGCCCTGGCTGAGGTACCTTCCGCAACCCCTGTCATTGAGAGGATTCCTC  
 GGCTCCGACGGCAGAAGAAAATTCTCAAGCAGCAAGGGAGGGCTTCCAGCGTGTAGGCAGATGAA  
 CATCGATGTCGCCACGTTGGCTGCTCCGGAGGTCATCCCCATGCCACGGGCACAGGCACCTT  
 AGCCCTGGGGCTTCTCCAGGATCCGAGGCCGGACCACGGGTGACATATCGGTGGAGAACGCTAACCTCG  
 GCACTGACTCGGACAGCTCACCTCAGAAGAGCTCGCGGATCCTCCAGCCATCGAGCCTGAGCTC  
 CCCCATCCAGGAATCCACTGCTCCCGAGCTGCCCTGGAGACCCAGGAGACCCCAGGCCCTGTGC  
 AGCCCTCTGAGGAAGTCACCTCTGACCCCTCGAAGATTCAAGTTCTGGCTGCTGGCCGGTCATT  
 TTGGGAAGGTGCTCCTCTCGAATTCCGGCCCAGTGGGAGCTGTTGCCATCAAGGCTCTGAAGAAAGG  
 GGACATTGTCGGCCCGAGACGAGGTGGAGAGCCTGATGTTGAGAACAGGGATATTGGCGGCAGTGACAGT  
 GCGGGACACCCCTCTGGTGAACCTCTCCGGCTTCCAGACACCGGAGCACGTGCTCGTGTGATGG  
 AGTACTCGGGCGGTGGGACCTGATGCTGCACATCCACAGCGACGTGTTCTGAGCCCCGTGCCATCTT  
 TTATTCCGCTCGTGGTCTGGCCTACAGTTCTCACGAACACAAGATGTCACAGGGACCTGAAG  
 TTGGACAATTGCTCCTGGACACCGAGGGCTACGTCAAGATGCAAGACTTGGCCTCTGCAAGGAGGGGA  
 TGGGCTATGGGACCGGACCAGCACATTCTGGGACCCGGAGTTCTGGCCCTGAGGTGCTGACGGA  
 CACGTCGTACACCGGAGCTGTTGGACTGGTGGGACTGGGTGCTGCTCACGAGATGCTGGTGGCAG  
 TCCCCATTCCCAGGGGATGATGAGGAGGGCTTCGACAGCATCGTCAACGACGAGGGCTCGTACCCCC  
 GCTTCCTGTCGGCGAAGCCATCGGCATCATGAGAAGGCTGCTCGGAGGAACCCAGAGCGGAGGCTGG  
 ATCTAGCGAGAGAGATGCAAGAGATGTAAGAAACAGCCCTCTCAGGACTCTGGGCTGGGAAGCCCTG  
 TTGGCCCGGGCCTGCCACCGCCCTTGTGCCACGCTGTCCGGCGACCGACGTCACTTCGAC  
 AGGAGTTCACCGGGAGGCCCCACACTGAGCCCACCGCGACCGCGGGCCCTCACAGCCGCGAGCA  
 GGCAGCCTCCTGGACTTCGACTCGTGGCCGGGGCTGCTAGCCCCCTCCCCCTGCCCTGCC  
 CTGCCCGAGAGCTTAAAGGCCATTGGGATTGCGGAAAAAAAAAAAAAA

>gi|4506073|ref|NP\_002732.1| protein kinase C-like 1; serine-threonine kinase N [Homo sapiens] (SEQ ID NO:31)  
 MASDAVQSEPRSWSLLEQLGLAGADLAAPGVQQLELERERLRREIRKELKLKEGAENLRRATTDLGRSL  
 GPVELLLRGSSRRLDLLHQQLQELHAHVVLDPAAATHDPQSPGAGGPTCSATNLSRVAGLEKQLAIELK  
 VKQGAENMIQTYNSNGSTKDRKLLLTAQQLQDSKTKIDIIRMQLRRALQADQLENQAAPDDTQGSPDLGA  
 VELRIEELRHHFRVEHAVAEAKNVRLLLSAAKAPDRKAVSEAQEKLTESNQKLGLLREALERRLGELPA  
 DHPKGRLLREELAAASSAAFSTRLAGPFPATHYSTLCKPAPLTGTLERVRVVGCRDLPETIPWNPTPSMGG  
 PGTPDSRPPFLSRPARGLYSRSGSLGRSSLKAEAENTSEVSTVLKDNTVVGOTSWKPCGPNAWDQSFT  
 LELERARELELAFLWFRDQRGLCALKFLKLEDFLDNERHEVQLDMEPQGCLVAEVTFRNPVIERIPRLRRQ  
 KKIFSQQGKAFQRARQMIDVATWVRLRRLIPNATGTGTFSPGASPGSEARTTGDISVEKLNLGTDSD  
 SSPQKSSRDPSSPSSLSSPIQUESTAPELPSETQETPGPALCSPLRKSPLTLEDFKFLAVLGRGHFGKVL  
 LSEFRPSGELFAIKALKGDIVARDEVESLMCEKRILAATVSAGHPFLVNLFGCFQTPEHVCFVMEYSAG

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GDLMLHIHSDFSEPRAIFYSACVVLGLQFLHEHKIVYRDLKLDNLLLDTEGYVKIADFGLCKEGMGYGD  
RTSTFCGTPEFLAPEVLTDTSYTRAVDWGLVLLYEMLVGESPPFGDDEEVFDISVNDEVRYPRFLSA  
EAIGIMRLLRRNPERRLGSSERDAEDVKKQPFFRTLGEALLARRLPPPFPVPLSGRTDVSNFDEEFTG  
EAPTLSPPRNDARPLTAAEQAAFLDFDVAGGC

Zip kinase

GH1-68-PCR-G3F1 (SEQ ID NO: 32)

GCTGGGTTTCATTCGAGTATTGGCGGGCTGCTCTCAGTAGGTTAGCCGTCGTGACCCCTCACGTGCACTCG  
TGGTCACTGTGGCACCGTGAGGGTTGGGACCCACCGAGGCGAAGGCGCCGAATGCGCTGTTCAAGCCGGAGAGG  
TTTGCCTGGTAGTTGCCGACATTGGCGGGTGTGCTGCTGCCATTATGCCAGGAGGAGGTGTGGACGG  
GGAGGGTGGGATGGACGGCGGACAGGAGTCCCACGCTGCTTGGTGGCGCCGGCTTGGTGGGGCTTCCACTGTGT  
GCCCTCTGCCGAGGGCGGTCCCCCGCTGTGGGGTGCCTGCGGACTCCTCCGACCGAGAAACCACGAC  
AGTGGTTAGAGTAGATAAAGCGGGCGAGTCGACTAGATCTGAGGTCTGATACTCACTGACTGTTCTGAA

>gi|4557510|ref|NM\_001348.1| Homo sapiens death-associated protein kinase 3  
(DAPK3), mRNA (SEQ ID NO: 33)

GTGCCATTAGGGACTCCTGAGGTCTATCTCAGGCTGCGGTGACTGCACTTCCCTGGAGTGGAAAGC  
TGCTGGAAGCGGGACCGGCCCATGTCCACGTTCAAGGAGTGGAGGACATTATGAGATGGG  
GGAGGAGCTGGCAGCGGCCAGTTGCATCGTGCAGGAAAGTGCAGGGCAGAAGGGCACGGCAAGGAGTAC  
GCAGCCAAGTTCATCAAGAACGCGGCCTGTCATCCAGGCCGTGGGGTGAAGCCGGAGGAGATCGAGC  
GGGAGGTGAACATCCTGCCGGAGATCCGGCACCCAAACATCATCACCTGCAAGACATCTCGAGAACAA  
GACGGACGTGGCCTCATCTGGAGCTGGTCTCTGGGGAGCTTGTACTTCCCTGGGGAGAAAGAG  
TCGCTGACGGAGGACGAGGCCACCAAGTCTCAAGCAGATCTGGACGGCTTCACTACCTGCACTCTA  
AGCGCATCGCACACTTGACCTGAAGCCGAAACATCATGCTGTTGACAAGAACGTGCCAACCCACG  
AATCAAGCTCATCGACTTGGCATCGCACAAGATCGAGGCGGGGAACGAGTTCAAGAACATCTCGGC  
ACCCGGAGTTGTGGCCCCAGAGATTGTGAACTATGAGCCGCTGGGCTGGAGGCGGACATGTGGAGCA  
TCGGTGTATCACCTATCTCTGAGCGGTGCACTCCCGTTCTGGGAGACCAAGCAGGAGACGCT  
CACCAACATCTAGCCGTGAACACTCGACTCGACGAGGAGTAACCTCAGCAACACCAGCGAGCTGGCAAG  
GACTTCATTGCCGGCTGCTCGTCAAAGATCCAAGCGGAGAATGACCATTGCCAGAGCCTGGAACATT  
CCTGGATTAAGCGATCCGGCGCGAACGCTGCGTGGTGGAGGACAGCGGCCAAGCCGAGCGCGCG  
CCTGAAGACACCGCTGAAGGAGTACACCCTCAAGTCGCACTCCAGCTTCCGCCCCAACACAGCTAC  
GCCGACTTCGAGCGCTTCCAAGGTGCTGGAGGAGGCCGCGCCGAGGAGGGCTGCGAGCTGC  
AGCGCAGCCGGCGCTGCCACGAGGACGCTGGAGGCGCTGGGCCATCTACGAGGAGAACGGCTG  
GTACCGCAGGAGAGCGACAGCCTGGCCAGGACCTGCGGAGGCTACGGCAGGAGCTGCTCAAGACCGAG  
GCGCTCAAGCGCAGCGCAGGAGGAGGCCAAGGGCGCTGCTGGGGACCAAGCGGCCCTCAAGCGCGCT  
TCAGCCGCTGGAGAACCGCTACGAGGCGCTGGCCAAGCAAGTAGCCTCCGAGATGCGCTTGTGAGGA  
CCTCGTGCAGCCCTGGAGCAGGAGAACGCTGAGGGCGTGGAGTGGGGCTGCGCTAGGCGCAGTGGGGT  
GGGCCAGGCCCCAGGACAGCGAGCTCGGCCAGGCTGGGGCGCTTCTGTGGACGCTGCGCTTCCA  
TCGCCCGGGTGCCTGTCTGCCAGCGCACCAGGCTGGAGGAGGAGCTGGAGGAGCTGGAGGCCAGGCC  
CGTAAGTTCGCAAGGAGGGGTGGTGTGGAGGGCTGCTTCTACACAGCCTCTACGCTGGCTTCA  
CCTTCACCCCTGCATCGTGGTGAACCTGGGACCCCTCAGGAGCGCTGGGCCATCTGAGGGTTG  
GGACCCACCGAGGCGCAGAGGCCGAATGCAAGCCCTGGTCAAGGCCGGAGGAGGGTTGCGGGTAG  
TTGCACGGACAATTGGCGGGGTGCTGCCAGGCTGGTGTGCTGCCATTAGCCAGGAGGAGGTGGAGGCC  
GGGTGGGATGGACGGCGGACAGGAGTCCCACGCTGCTGGTGGCGCCGGCTTGGTGGGGTCTTCCAC  
TGTGTGCCCTCTGCCGAGGCCGGTCCCCGGTGTGGGTGCCCTGCTGCCACTCCTCCGAGGCC  
CATCGTGCAGCCCTGTGGACGCCCTAGGCAAGAGGCCCTCTGCAAGCCAAGAGAAATAACTGGCTTC  
CAGAT

>gi|4557511|ref|NP\_001339.1| death-associated protein kinase 3 [Homo sapiens]  
(SEQ ID NO: 34)

MSTFRQEDVEDHYEMGEELGSGQFAIVRKCRQKGTKEYAAFKRRLSSSRGVSEEIEREVNLRE

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IRHPNIITLHDIFENKTDVVLILELVS GGELFDLAEKESLTEDEATQFLKQILDGVHYLHSKRIAHFDL  
 KPENIMLLDKNVPNPRIKLIDFGIAHKIEAGNEFKNIFGTPEFVAPEIVNYEPLGLEADMWSIGVITYIL  
 LSGASPFLGETKQETLTNISAVNYDFDEEYFSNTSELAKDFIRRLVKDPKRRMTIAQSLEHWSWIKAIRR  
 RNRGEDSGRKPERRRLKTTRLKEYTIKSHSSLPPNNSYADFERFSKVLEEEAAEGLRELQRSRRLCH  
 EDVEALAAIYEEKEAWYREESDSLQDRLRLRQELLKTEALKRQAQEEAKGALLGTSGLKRRFSRLENRY  
 EALAKQVASEMRFVQDLVRALEQEKLQGVECGLR

>gi|2911155|dbj|AB007144.1| Homo sapiens mRNA for ZIP-kinase, complete cds  
(SEQ ID NO:35)

GTTGCCATTAGGGACTCCTGAGGTCTATCTCCAGGCTCGGTGACTGCACCTTCCCTGGAGTGGAAAGC  
 TGCTGGAAGCGGACCGGCCATGTCCACGTTCAAGGAGCTGGAGGACATTATGAGATGGG  
 GGAGGAGCTGGCAGCGGCCAGTTGCATCGTGGAAAGTGCAGGAGCTGGAGGACATTATGAGATGGG  
 GCAGCCAAGTCATCAAGAACGCGCCGCTGTCACTCCAGCCGGCTGGGGTGAAGCCGGAGGAGATCGAGC  
 GGGAGGTGAACATCCTGCGGGAGATCCGGCACCCAACATCATCACCCCTGCACGACATCTCGAGAACAA  
 GACGGACGTGGCTCTCATCCTGGAGCTGGCTCTGGGGAGCTTTGACTTCCTGGCGAGAAAGAG  
 TCGCTGACGGAGGACGAGGCCACCCAGTTCTCAAGCAGATCTGGACGGCTTCACTACCTGACTCTA  
 AGCGCATCGCACACTTGACCTGAAGCCGGAAACATCATGCTGCTGACAAGAACGTGCCAACCCACG  
 AATCAAGCTCATCGACTTCGGCATCGCGACAAGATCGAGGCGGGAACGAGTTCAAGAACATCTCGGC  
 ACCCGGAGTTGTGGCCCAGAGATTGTGAACATATGAGCCGCTGGGCTGGAGGCGGACATGTGGAGCA  
 TCGGTGTCATCACCTATATCCTCTGAGCGGTGACATCCCCGTTCTGGCGAGACCAAGCAGGAGACGCT  
 CACCAACATCTCAGCCGTGAACTACGACTTCGACGAGGAGTACTTCAGCAACACCAGCGAGCTGGCCAAG  
 GACTTCATTGCCGGCTGCTCGTCAAAGATCCAAGCGGAGAATGACCATTGCCCAGAGCCTGGAACATT  
 CCTGGATTAAGGCATCCGGCGGGAACGTGCGTGGAGGACAGCGCCGCAAGCCGAGCGGGCG  
 CCTGAAGACCAACCGCTGAAGGAGTACACCATCAAGTCGACTCCAGCTTCCAGGACAGCGCCCAACAACAGCTAC  
 GCCGACTTCGAGCGCTCTCCAAGGTGCTGGAGGAGGCGGGCCGAGGAGGGCTGCGCGAGCTGC  
 AGCGCAGCGCCGCTCTGCCACGAGGACGTTGGAGGCGCTGGCCCATCTACGAGGAGAAGGAGGCCTG  
 GTACCGCGAGGAGAGCGACAGCCTGGCCAGGACCTCGGGAGGCTACGGCAGGAGCTGCTCAAGACCGAG  
 GCGCTCAAGCGGCAGGCCAGGAGGAGGCCAAGGGCGCGTGTGGGGACAGCGGCCCTAAGCGCCGCT  
 TCAGCCGCTGGAGAACCGCTACGAGGCGCTGGCCAAGCAAGTAGCCTCCAGAGATGCGCTTGTGAGGA  
 CCTCGTGCAGCCCTGGAGCAGGAGAAGCTGCAAGGCGTGGAGTGCAGGCTGCGCTAGGCGAGTGGGT  
 GGGCCAGGCCAGGACAGCGGAGCTGGCCTGCGTGGGGCGCTTCTGTGGACGCTGCGCCCTCCA  
 TCGCCCGGGTGCCTGTCTGGCCAGCGCCACCAGGCTGGAGGCGGAGTGGAGGAGCTGGAGGCCAGGCC  
 CGTAAGTTCGCAAGGCAGGGGTGGGTGTGGGACGGGGCTGCTCTACACAGCCTACGCTGGCCTTCA  
 CCTCACCCCTGCATCGTGGTGAACCTGGACCCCTCAGGCAGCGTGGCCTGTGGCACCGTGAGGGTT  
 GGACCCACCGAGGCGCAGAGCGGCCGAATGCAGCCCTGGTCAGGCCGGAGGAGGGTTGCGGGTAG  
 TTGCA CGGACAATT CGCGGGGTGCTGCCTGTTGCTGCCATTAGCCAGGAGGAGTGTGGAGGCCAGGGGA  
 GGGTGGGATGGACGGCGGACAGGAGTCCCAAGCCTGCTGGGTGGCAGGGCTTGGTGGGGTCTTCCAC  
 TGTGTGCCCTCTGCCAGGGCGGCTGGGGTGTGGGCTGCCCTGCTGCGACTCCTCCGAGGCC  
 CATCGTGCAGCCCTGTGGACGCTAGGCAAGAGCGGCCCTGCAAGCCAAGAGAAATAACTGGCTTC  
 CAGAT

>gi|2911156|dbj|BAA24955.1| ZIP-kinase [Homo sapiens] (SEQ ID NO:36)  
 MSTFRQEDVEDHYEMGEELSGQFAIVRKCRQKGTGKEYAKFIKKRLLSSRRGSREEIEREVNILRE  
 IRHPNIITLHDIFENKTDVVLILELVS GGELFDLAEKESLTEDEATQFLKQILDGVHYLHSKRIAHFDL  
 KPENIMLLDKNVPNPRIKLIDFGIAHKIEAGNEFKNIFGTPEFVAPEIVNYEPLGLEADMWSIGVITYIL  
 LSGASPFLGETKQETLTNISAVNYDFDEEYFSNTSELAKDFIRRLVKDPKRRMTIAQSLEHWSWIKAIRR  
 RNRGEDSGRKPERRRLKTTRLKEYTIKSHSSLPPNNSYADFERFSKVLEEEAAEGLRELQRSRRLCH  
 EDVEALAAIYEEKEAWYREESDSLQDRLRLRQELLKTEALKRQAQEEAKGALLGTSGLKRRFSRLENRY  
 EALAKQVASEMRFVQDLVRALEQEKLQGVECGLR

>gi|5162883|dbj|AB022341.1| Homo sapiens mRNA for ZIP kinase, complete cds  
(SEQ ID NO:37)

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GCACTTCCCTGGAGTGGAAAGCTGCTGGAAGGCCGACCGGCCCATGTCCACGTTAGGCAGGAGGACG  
 TGGAGGACCATATTGAGATGGGGGAGGAGCTGGCAGCGGCCAGTTGCGATCGTGCAGAAGTGCAGGCA  
 GAAGGGCAGGGCAAGGAGTACGAGCCAAGTCATCAAGAACAGCAGGCCCTGTATCCAGCCGGCTGG  
 GTGAGCCGGAGGAGATCGAGCAGGGAGGTAAACATCCTGCGGGAGATCCGGCACCCAAACATCATCACCC  
 TGCACGACATCTCGAGAACAGACGGACGTTGCTCATCCTGAGCTGGCTCTGGGGAGCTCTT  
 TGACTTCCTGGCGAGAAGGAGTCGCTGACGGAGGAGGCCACCCAGTTCTCAAGCAGATCTGGAC  
 GGCAGTCACTACCTGCACTCTAACGCGATCGCACACTTGACCTGAAGCCGAAAACATCATGCTGCTGG  
 ACAAGAACGTGCCAACCCACGAATCAAGCTCATCGACTCGGCATCGCGACAAGATCGAGGCGGGAA  
 CGAGTTCAAGAACATCTCGGCACCCGGAGTTGTGGCCCCAGAGATTGTAACATATGAGCCGCTGGC  
 CTGGAGGCGGACATGTGGAGCATCGGTGTCATCACCTATATCCTCTGAGCGGTGCACTCCCCTGG  
 GCGAGACCAAGCAGGAGACGCTCACCAACATCTCAGCGTGAACGACTTCGACGAGGAGTACTTCAG  
 CAACACCAGCGAGCTGCCAACAGGACTTCATCGCCGGCTCTGCAAAGATCCAAAGCGGAGAATGACC  
 ATTGCCCAGAGCCTGAAACATTCTGGATTAAGGCATCCGGCGGAAACGTGCGTGGTGAAGGACAGCG  
 GCCGCAAGCCCAGCGGGCGCTGAAGACCACGCGCTGAAGGAGTACACCATCAAGTCGCACTCCAG  
 CTGCGGCCAACAACAGCTACGCCACTTCGAGCGCTCTCCAAGGTGCTGGAGGAGGCCGGCGGCC  
 GAGGAGGGCTGCGAGCTGAGCGCAGCCGGCGCTCTGCCACGAGGACGTTGGAGGCGCTGGCGCCA  
 TCTACGAGGAGAAGGAGGCGCTGGTACCGCGAGGAGGCGACAGCTGGCCAGGACCTGCGGAGGCTACG  
 GCAGGAGCTGCTCAAGACCGAGGCGCTCAAGCGGCAGGCGCAGGAGGAGGCAAGGGCGCCTGGGG  
 ACCAGCGGCCTCAAGCGCCCTCAGCCGCTGGAGAACCGTACGAGGCGCTGGCCAAGCAAGTAGCCT  
 CCGAGATGCGCTTCGTGCAAGGACCTCGTGCAGCCCTGGAGCAGGAGAACGCTGCAGGGCGTGGAGTGC  
 GCTGCGCTAGGCGCAGTGGGTGGCCAGGCCCCAGGACAGCGAGCTGCCCTGCGGAGGCGCT  
 CCTGTGGACGCTGCGCCTCCATCGCCGGGTGCCTGCTGCCAGCGCCACCAGGCTGGAGGCGAG  
 TGGGAGGAGCTGGAGGCCAGGCCGTAAGTCGCAAGCAGGGTGGGTGTTGGACGGGGCTGCTCTAC  
 ACATCCTCCACGCTGGCTTCACCTCACCCCTGCACTCGTGCAGGACCTGGGACCCCTCAGGCAGCGT  
 GCCTGTGGCACCGTGAGGGTGGGACCCACCGAGGCGAGAGGGCCCGAATGCAGCCCTGGTTAGGC  
 CCGGAGGAGGGTTGCGGGTAGTTGCACTGGCAGGGTGCTGCCCTGCTGCCATTAGCCCA  
 GGAGGAGGTGCTGGGACGGGGAGGGTGGGATGGACGGGGACAGGCAGTCCCCACGCTGCTGGGTC  
 CGGGCTGGGGTCTTCACTGTGTGCCCTCTCGCGAGGCCGGTCCCCGGGTGGGGTGGGGTGCCTG  
 CTGCGGACTCTCCCGAGCCCCATCGCGCCTGTGGACGCCAGGCAAGAGCGGCCCTCTGCAGCCA  
 AGAGAAATAAAATACTGGCTCCAG

>gi|5162884|dbj|BAA81746.1| ZIP kinase [Homo sapiens] (SEQ ID NO:38)  
 MSTFRQEDVEDHYEMGEELGSGQFAIVRKCRQKGTKEYAKFIKKRRLSSRRGVSEEEREVNLRE  
 IHPNIIITLHDIFENKTDVVLILELVSGGELFDLAEKESLTEDEATQFLQIILDGVHLYHSKRIAHFDL  
 KPEINMLDKNVNPRIKLIDFGIAHKIEAGNEFKNIFGTPEFVAPEIVNYEPLGLEADMWSIGVITYIL  
 LSGASPFLGETKQETLTNISAVNYDFDEEYFSNTSELAKDFIRRLVKDPKRRMTIAQSLEHHSWIKAIRR  
 RNRGEDSGRKPERRRLKTRLKEYTIKSHSSLPPNNSYADFERFSKVLEAAAAEGLRELQRSRLCH  
 EDVEALAAIYEKEAWYREESDSLQDLRRLRQELLKTEALKRQAQEEAKGALLTSGLKRRFSRLENRY  
 EALAKQVASEMRVQDLVRALEQEKLQGVECGLR

Gas6

GH1-50-PCR-G3F1 (SEQ ID NO:39)  
 GCGCAGGAATCTGGTCATCAAGGTCAACAGGGATGCTGTCATGAAAATCGGGTGGCCGGGACTTGTCCAACCG  
 AGCGAGGACTGTATCATCTGAACCTTACCGTGGGAGGTATTCCCTCATGAGAACGACTACGTGCAGCTATAAAC  
 CTCGTCTGGATGCTGCACTGAAGAGCGCGCAGAACAC

>gi|4557616|ref|NM\_000820.1| Homo sapiens growth arrest-specific 6 (GAS6),  
 mRNA (SEQ ID NO:40)  
 CGCGAGCCGCCGCCGCCGCCGCCGATGTGACCTTCAGGGCCGCCAGGACGGGATGACCGGAGCCT  
 CGGCCCCGGCGCCGCCCTCGCCTCGGCCCTCCGGGCGCTCTGACCGCGCTCCCCGGCCATGGCC  
 CCTTCGCTCTGCCCGGGCCCGCCCTCGCGCGCGCAGCTGCTGCTGGCCCG

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AGTGC CGC GCT TGC CG CG CT GTT GCC GG CG CG GAGG CAC GC AGT CCT GCG CCC AGG CAG GC CG CG CG  
 CTT CAGG TCT CG AGG AGG CA AGC AGG CC AC CT GG AG AGG AG CT GT GC AG CC CG  
 GAGG AGG CG CG GG AGG TGT CG AGA AC G ACC CG AGA CG GATT AT TT ACCA AGA TACT TAG ACT GCA  
 TCA ACA AGT AT GGG TCT CG TA CACC AAA ACT CAGG CT CG CC AC CT CG GT GC AAA AC CT CG CT GACCA  
 GTG CAC G CCA ACC CG CG AT AGGA AAGGG ACCA AGC CT CG CC AGG AC CT AT GGG CA ACT TCT CT GCG  
 CT GT GT AA AG CT GG CT GGG GGG CG CT CG AGA CA AA AG AT GT CA AC GA AT GC AG CC AGG AGA AC GGG  
 GCT GCG CT CC AG AT CT GCG AC AACA AG CG GG TAG CT CC ACT GT TCC CT GCG AC AG CG GG CT CG AG CT CTC  
 CT CT GT AG GG CAGG AC CT GCG AC AG AC AT AG AC GAG TCG CAG ACT CG GAGG CT CG GGG GAGG CG CG CT GCG  
 AAG AAC CT GCG CG CT CT ACT CT GCG CT GT GAC GAGG CT TG CG TA CAG CT CC AGG AGA AGG CT  
 GCC GAG AT GT GG AC GAG TGT CT GCG AGG CG CT GT GAG CAGG CT CG GT GACT CCC AGG AG GCT AC AC  
 CT GCG AC CT GT GAC GGG CG TGG GGC CT CA AG CT GT CC AGG AC AT GG AC AC CT GT GAG GAC AT CT GCG  
 TG CG TGC CCT TCA CG CG TGG CA AG AGT GT GAG TCT GT TAC CT GGG CG GAT GT TCA GT GGG AC CCG  
 TG AT CC GACT CG CG CT CA AG AGG CT GCG AG CCG ACC AGG CT GG TAG CT GAG TT GACT TCC GG AC CTT GA  
 CCC CG AGG GCA T CTC CT CT T GCG GAG GCG ACC AGG AC AG CAC CT GG AT CG T GCT GCG CT GAG AG CC  
 GGC CG CG CT GG GAG CT GCG AG CT GCG CT AC AC CG GT GCG CG GT GCG ACC AG CAG CG GCG CG GT CAT CA ACC  
 AT GG CAT AT GT GG CAG AC AAT CT GT GT GAG GAG CT GG CG CG AAT CT GG T CAT CA AGG TCA AC AGG GAT GCG  
 TG T CAT GAA AAT CG CG GT GG CG GGG ACT TT G T CA ACC CG GAG CG GAG GACT GT AT C AT CT G A AC CT G ACC  
 GT GGG AGG T AT TCC CT CC AT GAG AAG GAC CT GT GCG CT AT AA ACC CT GT CT GG AT GG CT GCG AT GA  
 GG AG CT GG AACT GG CT GAG CG AGA AG AC ACC ACC AT CC AGG AA AC GG T GAA AGT G A AC AC GAG GAT GCG  
 GT GCT T CT CG GT GAC CG GAG AG AGG CT TTT CT ACC CCG G GAG CG CG CT CG C CT TCA CG C CT GG ACT AC  
 AT GCG GAC CCT CT GG AC GT CG GG ACT GA AT CA AC CT GG AAG T AG A AGT CG T G G CT CA CAT CG G C C AG  
 CG CAG AC AC AG CG CG GT CT GT TT GCG CT TGG G C C CG AC CT CC CG T GCG CT GCG CT CT CT GT G G C ACT  
 GGT AG ACT AT C ACT CC AC GA AG A A ACT CA AG A AG CAG CT GG T GT CT GG CG T G GAG C AT CG G C CT G  
 G C C T A AT GG GAG AT CA AGG T CT GCG AC CG C A AG AG CAG CT GG T C ACC G T CT GCG T GAG G GAG CG GT GAG  
 CC ACC CT GG AGG T GG AC GG C ACC AGG G G C A GAG CG GAG GT GAG CG CG CG CAG CT GCG AG GAG AG G G C T G G C  
 CG T GCG T GAG AGG CAC CT GCG GAG C C C G T G C T CAC CTT GCT GCG G G C T G C CAG AT GT GCG G G T G ACT  
 TCAG CG CC AGT CAC CG CG TT TAC CG CG G G C T G C AT G A C AT GG AG GT CA ACC CG GAG G C T G CT GG AC CT GG  
 ACG AGG CG CG GT ACA AG C AC AG CG AC AT CA CG G C C A C T C CT G C C C C C G T G G AG G C C G C C G C A G C T A  
 G G C C C C A C C G G A C G C G G C A G G C T T C T CAG T CT G T C C G A G A C A G C C G G G A G G C T G G G G C T C C T C  
 ACC AC GT GGG G C C AT GCT GAG AG CT GGG T T C C T CT G T G ACC AT C C G G C T G T A C A T AT CT G T A A AT  
 AGT GAG AT GG ACT T GGG C C T G AC G C C G C G C A C T C A G C C G T G G C C G G G G G A G G C C G C G C A  
 GCG CAG AG CG G G C T G A A G A A A T A A T T C T A T T A T T A C C A A G C G C T T C T G A C T C T A A A  
 AT AT GG A A A A T

>gi|4557617|ref|NP\_000811.1| growth arrest-specific 6; AXL stimulatory factor  
 [Homo sapiens] (SEQ ID NO:41)  
 MAPSLSPGPAA LRRAPQLL LAAECAL A ALL PARE AT QFLRPRQRRAFQVFEEAKQGHLE REC VEELC  
 SREEAREV FENDP ETDYF PRYL DCINKY GSPYTKNSGFATCVQNL PDQCTPNPCDRKG TQACQDLMGNF  
 FCLCKAGWGRLCDKD VNECSQENG CLQIC HNKPGSFHC SCHSGFELSSD GRT CQDI DECAD SEAC GEA  
 RCKNLPGSYSCLC DEG FAYSSQE KAC RDV D ECLQGRCEQVCVNSPGSYTCHCDGRGGLKLSQDM DT CEDI  
 LPCVPFSVAKSVKSLYLG RMFSGTPVIRLRFKRLQPT RLVAEFDFTFDPEGI LLFAG GHQDSTWIVL AL  
 RAGR LE LQLRYNGVGRVTSSGPVNHGMWQTISVEELARNLVKVN RDA VMKIAVAGDLFQPER GLYHLN  
 LTVGGIPFH EKDLVQ P IN PRLD GCMRS WNW LNG EDTT I QETVKVNTRM QCF SVTERGSF YPGSGFAFYSL  
 DYMRTPLDV G TESTWE VEVVAH IRPA ADT GVL FALWAPD LRAVPLSVALVDYHSTKKLQLVV LAVEHT  
 ALALMEIKVCDGQEHV VT VSL RDGE AT LEV DGTRG QSEV SAAQLQERLAVLERHLRSPVLT FAGGLPDV P  
 VTSAPVTA F YRG CMT LEV NRLL D EAAY KHSD ITA HSCPP VEPAAA

SRm160

GH1-67-PCR-G3F1 (SEQ ID NO:42)

GGTCTCTCTCGTCGCTT CCCCCTT CAGG CCT GCG CCA AAC CT GCA AG CCCC  
 AGA AG CC ACC CCG TCG AG CG GAG GT CCG CAG CCCC GGA AG CCA ATA ACT CC CT CAG GGG ACT CT CG GT CC CT CAG

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CTACTCGCCTGTGGAGCGTCGCCGTCCCTGCCCTCACACAGGGACCAGCAGCAGCAGCAGTGA  
GTCGCCGGAGAGGCCAGCGTGGGACAGCCGCTCCCCAGCCACAAGCGCAGAGGAGACACCTAG  
AGACACCCTCCAGGTCTCCATAAAATTGTCTTGAGGGATTNCACCACACCCTGCTTGA  
GTCCTTCTCCCCAGAGAACCGTGAAGGTCTTGTCTGCCTCTTTAACCTNGCAGCCTTGATTGGAG  
GGCGTCCCCCTTTCCCTCCCCCTTTAG

>gi|19923465|ref|NM\_016333.2| Homo sapiens serine/arginine repetitive matrix 2 (SRRM2), mRNA (SEQ ID NO:43)

GCGGCCAGCGGGGTGCGAGTGGCGCAGTCGGAGGCCGTTGCGGCCCTGAGGAAGCGAGGAGCGTCG  
GCGTCGGCTGAGGCAGCGAGGCAGGGCGAGGCAGGGCGAGGCCGAGGGACTCGGGAGCTCGA  
GCAGCGCGCGCAAGACCTCTCCCCCTCGAGGCGGGCGAGGCAGGGAGCGGTGGTGGCTCCC  
CCCCGGCACGGGGCATGTACAACGGGATCGGCTGCCAGCAGCCCCGGGAGCGGACCAACGGCTACG  
TCCAGCGAACCTGTCCCTGGTGCAGGGCCGGGTGAGCGGCCTGACTACAAGGGAGAGGAGGA  
GCGGCGCCTGGAGGCTGCCCTGGTAAGCGGCTAACCTGACATCCTGACCACAGCGCAAGCGCG  
GTCGAGCTGCATGCCCTGAGCTGGAGGAGATGATGGAAGAGCAGGGTACGAGGAACAGCAAATCAG  
AAAAAGTGGCACCTTCGACTCATGTTGCTGGAGAAGGATGTGAACCTGGGGCAAGGAGGAGACCC  
AGGGCAGAGGCCAGCGTCACGGAGACTCACCAGTTGCAAGAATTAAATGAGAAGAAGAATGAAAGACTC  
CGTGCCTTGGCATCAGTGAATTCTACAGTGAAGCAGCTCTTGTACGCTGCGAGGAGTCTAGCAGTTCTCGCTC  
AAGCTAAACAAACCAGCTCCTGAGCCTCCAAACCTAACGCTTGTGGAGTCTAGCAGTTCTCGCTC  
ACCAACCCCAAAGCAGAAGAAGAAAAGAAGAAAGATAGAGGACGCGAGTCAGAGAGCAGCTCCT  
CGACGGGAGAGAAAGAAAAGCTCAAAGAAGAAGCACAGGTCAAATCTGAGTCCAAGAACGTAAGC  
ATAGGTCTCCACTCAAAGAGCAAACGTAATCTAAGGACAAAAGCGAAAGCGGTCTGAAGTACAAC  
ACCAGCCCCAAGAGCGCCGGGGCACCGTTCAACTCTGCTGACTCTGCTTCTCCGATACTCC  
CGCAGTCGGTCTCGAAGTGCAGCTAAACTCATACAACGCTTGGTGGCGAAGTCCTTCCCTG  
CTCAGGGCGACGCGGGAGGGAGATGCGCCTTCAGTGAACCAGGTACTACCAGCACACAACGGCTAG  
TAGCCCGAGACTGCTACGAAACAGCTAGCAGCCATTGAAGACAAAGATAAAAGACAAGAAGGAGAAA  
TCTGCAACTCGACCTAGCCCCCTCCGGAAAGGAGCAGCACAGGGCCAGAACCCACCTGCTCCCACCTCC  
TCCTGCTGAGCGACATGGCGCTCCCCACAACCCCTGCAACCACCCCTAAGCCAGGAGCCAGTGAA  
CCCCCATCTGAGGCCTCTCAAACCTGGGACCGTTACCACCTAAGTCTCCGAGAAACTCCCCAGTCT  
TCTCCTCAGAGAGCAGCCCACCATCCCCCTAACCTACCAAAGTTCTCGGATGCCAGCTTCCCCAG  
AAAGTCCTAACCTGCTCCAGCTCCAGGGTCCCACCGAGAGATTCTCTCCACATCTAAGAATCG  
CTCACATGGCGAGCAAACGGATAAAATCACATTCTCATACCCCTCCGTTAGGATGGGAGGTTCC  
AGCCCTGCCACCGCTAACAGAGAGGGCGATCTGGTCTCGAACCCCTACCAAGAGAGGTCTAG  
GATCTCCCAGTGGCTAGGTCCAGGTCTGCACAGAGGTGGGAAGATCTAGAACGCCCCAGCGACGTGG  
CCGCTCTAGGTCTCCTCAGCGACCAGGCTGGTAGGAGCAGAAATACCCAGAGAAGAGGCAGGTCTAG  
TCAGCAAGGGAGGGAGGTCCACTCTAGATCCCCAGCCACTAGGGTAGATCTCGTTCTAGAACACCCAG  
CCCGCCGGGGCAGGTCCGCTTAGAACACCTGCGAGCGGAGATCAGATCCAGAACCTCCACCGAGCG  
TAGGTCTGGTCTAGAACACACCAGGCCAGGGCAGGTCTCGGTCTAGAACACCTGCTAGGCGCAGATCT  
AGGACCCGATCACCAAGTACGACGCAAGGTCTCGTAGATCACCAAGCCAGGAGAACGTGGCAGGTACGCT  
CTAGAACCCAGCTAGACGTGGCGCTCACGCTCCAGAACACCAGCCAGGAGAGGGAGGTCTGGTCTAG  
AACCCAGCTAGACGCAAGTGGCGCTCACGCTCCAGAACACCAGCCAGGAGAGGGAGGTCTGGTCTAG  
ACACCAAGAGCAGGAAGATCCCCAGTAGAACAGCTTAGTTAGACGTGAAGATCTCACTCTAGAACACCTC  
AAAGAAGAGGCAGATCTGGCTCATCTTCAGAGCGGAAAAACAAATCCAGAACATCTCAAAGAAGAAGCAG  
GTCCAATTCAAGCCCAGAAATGAAGAAATCTCGCATTCTCAAGGGCGGAGCAGGTCTCTCTTCA  
CGGTCAAAGCAAATCTCGCTTGCTTGGAGCGCAGCCTTCAGGGTCTCCCCATGCCCTAACAAA  
AGTCACAGACACCACCCAGGCGCAGTCGCTCTGGATCTCCAAACCTAAAGCTAACATCTAGAACGCCACC  
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AGTATCTCCCTGCTCCAATGTGGAATCCAGATTGGTGCCTAAGATCAGTCATTCTGGGTCTCCCTCACCA  
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>gi|19923466|ref|NP\_057417.2| splicing coactivator subunit SRm300; RNA binding protein; AT-rich element binding factor [Homo sapiens] (SEQ ID NO:44)  
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 LELEEMMEEQGYEEQQIQEKVATFRLMLLEKDVNPGKEETPGQRPAVTETHQLAELNEKKNERLRAFG  
 ISDSYVDGSSFDPQRRAREAKQPAPEPPPKPYSLVRESSSRSPTRPKQKKKKKKDRGRRSSESSSPRRERK  
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FSASPMILKSGMSPEQSRFQSDSSYPTVDSNSLLGQRLETAESKEKMALPPQEDATASPPRQDKDFSPF  
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>gi|6649241|gb|AF201422.1|AF201422 Homo sapiens splicing coactivator subunit SRm300 (SRM300) mRNA, complete cds (SEQ ID NO:45)  
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CCCCCCCCGGGACGGGCCATGTACAACGGGATCGGCTGCCGACGCCCGGGCAGCGCACCAACGGC  
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 TGGATGGAGGGCTCCCTTCCCTCCCTTCTTGTCTTGTGAAATGTTAATCTCGTGAGT  
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 GATACAGTTCAAGGATAACCCAGCCTGGAATTAGGGCAGGAAGCATGGCCCACTTGATCCAGAAGTT  
 ACCCAGGGGTGATTGTGATGGTGGTGGACTGGAGGGTGTATAAGGTGTTCTGAAAGGGAGTTGAAT  
 TAGTTGGTCCTACTGTCCCCATGAGGTTGTGAACCCCTCCCCCAACTTTCATGTTCTTAAAGGCA  
 TTTGGTTTTAAATCTGTACAGCAAGAGCAACTTTCTGTCAAATAAAATGAGAAATGCAGGAA  
 AAAAAAAAAAAAAAA

>gi|6649242|gb|AAF21439.1|AF201422\_1 splicing coactivator subunit SRm300  
 [Homo sapiens] (SEQ ID NO:46)  
 MYNGIGLPTPRSGTNVYQRNLSLVRGRGERPDYKGEELRRLEALVKRPNPDILDHERKRRVELRC  
 LELEEMMEEQYEEQQIQEKVATFRLMLLEKDVNPGKEETPGQRPAVTETHQLAELNEKKNERLRAFG  
 ISDSYVDGSFDPQRRAREAKQPAPPEPPKPYSLVRESNNRSRSPQSRKKRKIEDAGQRAALLGRER  
 KAQRRLSTGQNLSPRNVSIGLPLQRANVNLRKSESGLEVQHQPRAAGPTVQLLTLPPPILPAVGLE  
 VLQLKLQLPWLGEVLPPLLQGDAGREMRLSVNQVLSTQRASSPETATKQPSSPYEDKDKKKEKSATRP  
 SPSPERSSTGPEPPAPTPLLAERHGGSPQPLATTPLSQEPVNPPSEASPTRDRSPPKSPKLPQSSSES  
 SPPSPQPTKVSRHASSPESPKPAPAPGSHREISSSPSKNRSHGRAKRDKHSHTPSRRMGRSRSPATA  
 KRGRRSRSRPTKRGHRSRSRSPQWRRRSAQRWGRSRSPQRGRRSRSPQRPGWSRSRNTQRRGRSRARRG  
 RSHSRSPATRGRRSRTPARRGRRSRTPARRRSRSRTPTRRRRSRTPARRGRRSRSPARRRSRSPARRS  
 VRGRRSRSRSPARRGRRSRTPARRGRRSRTPARRGRRSRSPARRGRRSRSPARRGRRSRSPARRS  
 RSRSRSLVRRGRSHSRTPQRRGRSGSSSERKNKSRSTSQRGRSNSSPEMKKSRISSRRSRSLSSPRSKAK  
 SRSLRRSLSGSSPCPKQKSQTPPRRSRSGSSQPKAKSRPPRSRSSSSPPPQKSKTPSRQSHSSSP  
 HPKVSGTPPRQGSITSQANEQSVPQRSCFESSPDPPELKSRTPSRHSCGSSPPRVSSTPPRQSPS  
 RSSSPQPKVKAIISPRQRSHGSSSPSPSRVTSRTPRRSRSVSPCSNVESRLLPRYSHGSSSPDTKVK

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PETPPRQSHSGSISPYPKVKAQTPPGPSLSGSKSPCPQEKS KDSL VQSCPGS LSCAGVKSS T PPGESYF  
GVSSLQLKGQSQTSPDHRSDTSSPEVRQSHSESPSLQSKSQTSPKGGRSRSSSPVTELASRSPIQRDRGE  
FSASPMLKSGMSPEQS RFQSDSSYPTVDSNSLLGQRLETAESKEKMA LPPQEDATASPPRQDKFSPF  
PVQDRPESSLVFKD LRTPRERSGAGSSPETKEQNSALPTSSQDEELMEVVEKSEEPAGQILSHLSEL  
KEMSTS NFESSPEVEERPAVSLTDQS QS QAS LEAVEVPSMASSWGGPHFSP EHKELNSPLRENSFGSP  
LEFRNSGPLGTEMNTGF S SEVKE DNLNGPFLNQLETDP SLD MKEQSTRSSGHSSSELSPDAVEKAGMSSNQ  
SISSPVLDAVPRTPSRERSSSASSPEMDGLPRTPSRRSRSGSPGLRDGSGTPSRHSLSGSSPGMKDIP  
RTPS RGRSECDSSPEPKALPQT PRRRSRSPSSPELNNKCLTPQ RERSGSESSVDQKT VARTPLGQ RSRSG  
SSQELDVKP SASPQERSESDSSPD SKAKTRPLRQ RSRSGSSPEVDSK SRLSPRRSRGSSPEVKDKPRA  
APRAQSGSDSSPEPKAPAPRALP RRSRSGSSSKGRGPSP EGSSSTESSPEHPPKSRTARRGSRSSPEPKT  
KSRTPPR RRSR SSSPELTRKARL SRRS R SASSSPETRSRTPPR HRRSPSVSSPEPAEKSRSSRRRSASS  
PRTKTT SRRGRSPSPKPRGLQ RSR SR RREKTRT RRRDRSGSSQSTSRRRQ RSR SR SVTRRRGGSGY  
HSRSPARQESSRTSSRRRRGRSRTPPTSRK RSR SRTSPAPWKR SRSRAS PATHRRSR SRTPLISRRRSRS  
RTSPV SRRRSR SRTS VTRR RSR S RASP V SRRRSR SRTPPV T RRSR SRT P T RRSR SRT P P V T RRSR S  
RTPP VTRR RRSR SRTSPIT RRR RSR SRTSPV T RRSR SRTSPV T RRSR SRTSPV T RRSR SRT PPAQDQPR  
SPVPSAFSDQS RCLI A QT P VAGSQ LSSGA VATT T SAGDHNGML SVPAPGVPHSDVGEPPA STGAQQP  
SALAALQPAKERRSSSF PFPCKAWPSGL  
AQTCKPQEA TPWRAEVQPPEANRLPQGLS VPQOLLACGASPSLA PALT GPAEQQQ

Non-muscle myosin heavy chain

GH1-90-PCR-G3F1 (SEQ ID NO:47)

GCTCCCTAAAGAACAGCTCAGGC CGGGGACCTGCCGTTGT CGTGCCCCCGCGAATGCCCGGAAAGGCCGG  
GATGGCTCCGACGAAGAGGTAGATGGCAAAGCGGATGGGCTGAGGCCAACCTGCCAATAGCCTCTCCTGC  
AGCCTGAGATGGATGGACAGACAGCACACCAGCCTCCCC

>gi|22507396|ref|NM\_002473.2| Homo sapiens myosin, heavy polypeptide 9, non-muscle (MYH9), mRNA (SEQ ID NO:48)

ATGGCACAGCAAGCTGCCATAAGTATCTCATGTGGATAAAA ACTTCATCAACAATCCGCTGGCCAGG  
CCGACTGGCTGCCAAGAACGCTGGTATGGTGCCCTCCGACAAGAGTGGCTTGAGCCAGCCTCAA  
GGAGGAGGTGGCGAAGAGGCCATCGTGGAGCTGGTGAGAATGGGAAGAACGGTGAAGGTGAACAAGGAT  
GACATCCAGAACGATGAACCCGCCAAGTCTCCAAGGTGGAGGACATGGCAGAGCTACCGTGCCTCAACG  
AAGCCTCGGTGCTGCACAACCTCAAGGAGCGTTACTACTCAGGGCTCATCTACACCTATT CAGGCCTGTT  
CTGTGTGGTCATCAATCCTACAAGAACCTGCCATCTACTCTGAAGAGATTGTGGAAATGTACAAGGC  
AAGAAGAGGCACGAGATGCCCTCACATCTATGCCATCACAGAACCGCCTACAGGAGTATGCAAG  
ACCGAGAACGATCAATCCATCTTGCACTGGTGAATCTGGAGCTGGCAAGACGGAGAACACCAAGAACGGT  
CATCCAGTATCTGGCTACGTGGCTCTCCGACAAGAGCAAGAACGGACCAGGGCGAGCTGGAGCGCAG  
CTGCTGCAGGCCAACCCCATCTGGAGGCCCTCGGAACGCCAACGGCTGAAGAACGAAACTCCTCCC  
GCTTCGGCAAATT CATCGCATCAACTTGTCAATGGCTACATT GTGGAGGCCAACATTGAGACTTA  
TCTTTGGAGAAATCTCGTGTATCCGCCAAGCCAAGGAAGAACGGACCTCCACATCTTCTATTATCTC  
CTGCTCTGGGCTGGAGAGCACCTGAAGACCGATCTCTGTGGAGCCGTACAACAAATACCGCTCCTGT  
CCAATGGACACGT CACC ATCCCCGGCAGCAGGACAAGGACATGTTCCAGGAGACCATGGAGGCCATGAG  
GATTATGGGATCCCAGAACAGAGGAGCAAATGGGCTGCTGCCGCTCATCTCAGGGTTCTCAGCTCGGC  
AACATCGTCTCAAGAACGGAGCGAACACTGACCAGGGCTCCATGCCGACAACACAGCTGCCAAAAGG  
TGTCCCATCTCTGGGTATCAATGTGACCGATT CACCA GAGGAATCCTACCCCGCGCATCAAGGTGGG  
ACGGGATTACGTCCAGAACGGCGCAGACTAAAGAGCAGGCTGACTTTGCCATCGAGGCCCTGGCCAAGGCC  
ACCTATGAGCGGATGTTCCGCTGGCTGGTGCGCATCAACAAGGCTCTGGACAAGACCAAGAGGCAGG  
GCCCTCCTCATCGGATCCTGGACATTGCCGCTTGAGATCTTGATCTGAACCTGTTGAGCAGCAGCT  
GTGCATCAATTACACCAATGAGAACGCTGCAGCAGCTCTCAACCAACACCATGTTCATCTGGAGCAGGAG  
GAGTACCA CGCGAGGGCATCGAGTGGAACTT CATCGACTTGGCCTGACCTGCAGCCCTGCATCGACC  
TCATTGAGAACGCCAGCAGGCCCGGGATTCTGCCCTGCTGGACGAGGAGTGCTGGTCCCCAAAGC

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CACCGACAAGAGCTTCGTGGAGAAGGTGATGCAGGAGCAGGGCACCCACCCCAAGTTCCAGAACGCCAAG  
CAGCTGAAGGACAAAGCTGATTCTCATTATCCACTATGCCGGCAAGGTGGATTACAAAGCTGACGAGT  
GGCTGATGAAGAACATGGATCCCTGAATGACAACATCGCCACACTGCTCCACCAGTCTCTGACAAGTT  
TGTCTCGGAGCTGTGGAAGGATGTGGACCGCATCATCGGCTTGACCAGGTGGCCGGATGTCGGAGACC  
GCACTGCCGGGGCCTCAAGACCGGAAAGGCATGTTCCGCACTGTGGGGCAGCTTACAAGGAGCAGC  
TGGCCAAGCTGATGGCTACGCTGAGGAACACGAACCCCAACTTGTCCGCTGCATCATCCCCAACACGA  
GAAGAAGGCCGGCAAGCTGGACCCGATCTGTGCTGGACCAGCTGCGCTGCAACGGTTCTCGAGGGC  
ATCCGTATCTGCCGCCAGGGCTTCCCACACAGGTGGCTTCCAGGAGTTTCCAGGAGATATGAGATCC  
TGACTCCAAACTCCATTCCAAGGGTTCATGGACGGGAAGCAGGCAGTCGTGCTCATGATAAAAGCCCT  
GGAGCTCGACAGCAATCTGTACCCATTGGCCAGAGCAAAGTCTTCTCGTGCCTGCTGGCCAC  
CTGGAGGAGGAGCAGACCTGAAGATCACCGACGTCATAGGTTCCAGGCCTGCTGCAGGGCTACC  
TGGCCAGGAAAGCATTGCAAGCGGCAGCAGCAGCTTACGCCATGAAGGTCTCCAGCGGAACTGCGC  
TGCCTACCTGAAGCTGCGGAACTGGCAGTGGTGGCGCTTCACCAAGGTCAAGCCGCTGCTGCAGGTG  
AGCCGGCAGGAGGAGGAGATGATGGCAAGGAGGAGGAGCTGGTAAGGTCAAGAGAGAACGAGCTGGCTG  
CGGAGAACAGGCTCACGGAGATGGAGACGCTGAGTCAGCTCATGGCAGAGAAATTGAGCTGAGGA  
GCAGCTCCAGGCAGAAACGAGCTGTGTGCCAGGGCTGAGGAGCTCCGGGCCCTGACCGCCAAGAAG  
CAGGAATTAGAAGAGATCTGCCATGACCTAGAGGCCAGGGTGGAGGAGGAGGAGCCTGCCAGCACC  
TGCAGGCGGAGAAGAAGAACATGAGCAGCAGAACATCCAGGAGCTTGAGGAGCAGCTGGAGGAGGAGAG  
CGCCCGGAGAACAGCTGAGCTGGAGAACGGTACCACCGAGGCGAACGCTGAAAAAGCTGGAGGAGGAGCAG  
ATCATCCTGGAGGACCAACTGCAAGCTGCCAAGGAAAAGAAACTGCTGGAAGACAGAACATGAGT  
TCACCACCAACCTCACAGAACAGGAGGAGAAATCTAAGAGCCTGCCAAGCTCAAGAACAGCATGAGGC  
AATGATCACTGACTTGGAAAGAGGCCCTCCGAGGGAGGAGAACAGCAGCAGAGCTGGAGAACGCCGC  
CGGAAGCTGGAGGGAGACTCCACAGACCTCAGCAGCACATGCCAGCTCCAGGCCAGATGCCGGAGC  
TCAAGATGCACTGCCAAGAACAGGAGGAGCTCCAGGCCCTGGCAGACTGGAAGAGGAAGCTGC  
CCAGAACATGCCCTCAAGAACATGCCAGCTGGAGCTGAATCTCAGATCTGAACCTCAGGAAGACCTG  
GAGTCTGAGCGTGCTTCCAGGAATAAGCTGAGAACAGAACGGACCTGGAGAACAGCTAGAGGCTC  
TGAAAACAGAGTTGGAGGACACGCTGGATTCCACAGCTGCCAGCAGGAGCTCAGGTCAAAACGTGAGCA  
GGAGGTGAACATCCTGAAGAACGCCCTGGAGGAGGAGGCCAACGCCACGAGGCCAGATCCAGGAGATG  
AGGCAGAACGACTCACAGGCCCTGGAGGAGCTGGCGAGCAGCTGGAGCAGACGAAGCGGGTAAAGCAA  
ACCTCGAGAACGGCAAGCAGACTCTGGAGAACAGAGCAGGGGGAGCTGCCAACAGGGTAAGGTGCT  
GCAGGGCAAGGGACTCGGAGCACAAGCGCAAGAACAGTGGAGGCCAGCTGCAGGAGCTGCAGGTCAAG  
TTCAACGAGGGAGAGCCGTGCGCACAGAGCTGCCAGCAAGGTACCAAGCTGCAGGTGGAGCTGGACA  
ACGTGACCGGGCTCTCAGCCAGTCCGACAGCAAGTCCAGCAAGCTCACCAAGGACTTCTCGCGCTGGA  
GTCCCAGCTGCAGGACACTCAGGAGCTGCTGCAGGAGGAGAACGGCAGAACGCTGAGCCTGAGCAGCA  
CTCAAGCAGGTGGAGGACAGAACATTCTCCGGAGCAGCTGGAGGAGGAGGCCAACGACA  
ACCTGGAGAACGAGATGCCACCCCTCATGCCAGGTGGCCAGATGAAAAAGAACATGGAGGACAGTGT  
GGGTGCCCTGAAACTGCTGAGGAGGTGAAGAGGAAGCTCCAGAACGGACCTGGAGGGCCTGAGCCAGCG  
CACGAGGAGAACGGTGGCCCTACGACAAGCTGGAGAACAGAACAGCGGCCAGCAGGAGCTGGAC  
ACCTGCTGGTGACCTGGACCACCGAGCGCAGAGCGCTGCAACCTGGAGAACAGCAGAACAGTGTGA  
CCAGCTCTGGCGAGGAGAACAGGACATCTGCAAGTATGCAGAGGAGCAGGCCAGGGCTGAGGCCAG  
GCCGAGAACGGAGAACAGGCTCTGCGTGGCCGGCCCTGGAGGAAGCCATGGAGCAGAACGGCG  
AGCTGGAGCGGCTCAACAAGCAGTTCCGACGGAGATGGAGGACCTTATGAGCTCCAAGGATGATGTGG  
CAAGAGTGTCCACGAGCTGGAGAACAGCTGCCAGAGCGCAGCTGGAGGAGGAGATGAAGACGAG  
CTGGAGAGCTGGAGGAGCAGCTGCAAGGCCACCGAAGATGCCAGCTGCAGGTGGAGGAGATGAAGAC  
CCATGAAGGCCAGTTCGAGCGGACCTGCAAGGCCAGGAGCAGAGCAGAGCGAGGAGAACAGCAGCT  
GGTAGACAGGTGCGGGAGATGGAGGAGCAGAGCTGGAGGAGCAGAGGAGAACAGCGCTCGATGCCAGTGG  
GCCCGGAAGAACAGCTGGAGATGGACCTGAAAGGACCTGGAGGAGCAGACATGACTCGGCCAACAGAACCGGG  
ACGAAGCCATCAAACAGCTGCCAGCTGCAAGGCCAGATGAAGGACTGCACTGCGAGCTGGATGACAC  
CCGCCCTCTGAGGAGATCTGGCCAGGCCAACAGAACAGGAGAACAGGAGAACAGCAGAACAGCAGCT  
GAGATGATCCAGTTGCAAGGAGAACAGCAGGCCAACAGAACAGGAGGCCAGGAGCAGGCCAGGG  
ATGAGCTGGCTGACGAGATGCCAACAGCAGGCCAACAGAACAGGAGGCCCTGGCGTTAGAGGAGAACGCC  
GGAGGCCGATGCCAGCTGGAGGAGGAGCAGGGCAACACGGAGCTGATCAACGAC

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CGGCTGAAGAAGGCCAACCTGCAGATCGACCAGATCAACACCGACCTGAACCTGGAGCGCAGCCACGCC  
AGAAGAACGAGAACATGCTCGGCAGCAGCTGGAACGCCAGAACAAAGGAGCTTAAGGTCAAGCTGCAGGAGAT  
GGAGGGCACTGTCAAGTCCAAGTACAAGGCCCATCACCGCCCTCGAGGCCAGATTGCACAGCTGGAG  
GAGCAGCTGGACAACGAGACCAAGGGAGGCCAGGCAGCTGCAAACAGGTGCGTCGGACCGAGAACAGC  
TGAAGGATGTGCTGCAGGTGGATGACGAGCGGAGGAACGCCAGCAGTACAAGGACCAGGCCACAA  
GGCATCTACCCGCCTGAAGCAGCTCAAGCGGCAGCTGGAGGCCAGAGGAGGCCAGCGGGCCAAC  
GCCTCCCGCCGGAAACTGCAGCGAGCTGGAGGCCACTGAGACGCCAGTGCATGAACCGCGAAG  
TCAGCTCCCTAAAGAACAAAGCTCAGGCCGGGGACCTGCCGTTGCTGCCCCGCCGAAATGGCCCGAA  
AGGCGCCGGGGATGGCTCCGACGAAGAGGTAGATGGCAAAGCGGATGGGCTGAGGCCAAACCTGCCGAA  
TAAGCCTCTCTCCTGCAGCCTGAGATGGACAGACAGACACCACAGCCTCCCTCCCAGACCCCG  
CAGCACGCCTCTCCCCACCTTCTTGGACTGCTGTGAACATGCCTCCTGCCCTCCGCCAGTCCCC  
CATCCGTTCCCTCCAGGTGTTGAGGGCATTGGCTCCTCTGCTGCATCCCCTCCAGCTCCCTC  
CCCTGCTCAGAATCTGATACCAAGAGACAGGGCCCGGCCAGGCAGAGAGCGACCAGCAGGCTCCTCA  
GCCCTCTCTGCCAAAAGCACAAGATGTTGAGGCAGCAGGGCAGGCCGGGAGGGGCCAGAGTT  
TCTATGAATCTATTTCTCAGACTGAGGCCTTTGGTAGTCGGAGCCCCCGAGTCGTCAGCCTCC  
GACGTCTGCCACCAGGCCCACTCCTCCTTCTTGCTGTTGCAATCACACGTGGTACCTCAC  
ACACCTCTGCCCTTGGGCTCCACTCCATGGCTCTGGCGGTCCAGAAGGAGCAGGCCCTGGCCTC  
CACCTCTGTGCAGGGCACAGAACGGCTGGGGGGAGGAGTGGATTCTCCTCCACCTGTCCCAGGCA  
GCCCACTGTCCGCTGTCCTCCCTGATTCTAAATGTCCTCAAGTGAATGCCCTCCCTCCTTAC  
CGAGGACAGCCTGCCACAGCAAGGCTGTCGGGTCAAGCTGAAAGGCCAGCAGCCTCCAGTG  
GCTTCTCCAACACTCTGGGACCAAATATTTAATGGTTAAGGGACTTGTCCAAAGTCTGACAGCA  
GAGCCTAGAGGGCCAGGCCCTCCAGGCATCTGTCTACTCTAGGACTGGGCCAGGGTGGT  
TTACCTGCACCGTTGACTCAGTATAGTTAAAAATCTGCCACCTGCACAGGTATTTGAAAGCAAAATA  
AGGTTTCTTTTCCCTTCTGTAATAAATGATAAAATCCGAGTCTTCTCACTGCCTTGTTAG  
AAGAGAGTAGCTCGTCCACTGGCTACACTGGTGCGAATTACTGTATTCTAACTGTTGTAT  
ATGCTGCATTGAGACTTACGGCAAGAACGGCATTTTTTAAAGGAAACAAACTCTCAAATCATGAA  
GTGATATAAAAGCTGCATATGCCTACAAAGCTCTGAATTAGGTCCAGTTGCTGTCACAAAGGAGTGAG  
TGAAACTCCCACCCCTTTTATATAATAAAAGCTGCCTAGCATGTGTTGCAGCTGTCACCACT  
ACAGTAAGCTGGTTACAGATGTTTCCACTGAGCATCACAATAAGAGAACCATGTGCTACGA

>gi|12667788|ref|NP\_002464.1| myosin, heavy polypeptide 9, non-muscle [Homo sapiens] (SEQ ID NO: 49)

MAQQAADKYLVDKNFINNPLAQADWAAKLWVPSDKSGFEPASLKEEVGEEAIVELVENGKKVKVNKD  
DIQKMNPPKFSKVEDMAELTCLNEASVLHNLKERYYSGLIYTYSGLFCVVINPYKNLPIYSEEIVEMYKG  
KKRHEMPPHIYAITDTAYRSMMQREDQSILCTGESGAGKTENTKKVIQYLAVVASHKSKKDQGELEHQ  
LLQANPILEAFGNAKTVKNDNSRFGKFIRINFVDVNGYIVGANIETYILLEKSRAIRQAKEERTFHIFYYL  
LSGAGEHLKTDLLPEPYNKYRFLSNGHVTIPGQQDKDMFQETMEAMRIMGIPEEEQMGLRVisGVQLG  
NIVFKKERNTDQASMPNTAAQKVSHLLGINVTDTRGILTPRIKVGRDYVQKAQTKEQADFAIEALAKA  
TYERMFRWLVRINKALDKTRQGASFIGILDIAQFEIFDLNSFEQLCINYTNEKLQQLFNHTMFILEQE  
EYQREGIEWNFIDFGLDLQPCIDLIEKPAGPPGILALLDEECWFPKATDKSFVKEVMQEQQGTHPKFQKPK  
QLKDKADFCIIHYAGKVDYKADEWLMKNMDPLNDNIATLLHQSSDKFVSELWKDVDRIGLDQVAGMSET  
ALPGAFKTRGMFRVGQLYKEQIQLMATLRNTNPNVRCIIPNHEKKAGKLDPLHVLIDQLRCNGVLEG  
IRICRGFPNRVVFQEFRQRYEILTPNSIPKGFMDGKQACVLMIKALELDSNLYRIGQSKVFFRAGVLAH  
LEEERDLKITDVIIGFQACCRGYLARKAFAKRQQQLTAMKVLQRNCAAYLKLRNWQWWRFTVKPPLLQV  
SRQEEEMMAKEELVKVREKQLAAENRLTEMETLQSQLMAEKLQLQEQLQAETELCAEAELRARLTAKK  
QELEEEICHDLEARVEEEEERCQHQLQAEEKKMQQNIELEEEQLEEEESARQKLQLEKVTTEAKLKKLEEEQ  
IILEDQNCKLAKEKKLLEDRIAETTNLTEEEEKSLSIQLKNKHEAMITDLEERLRREEKQRQELEKTR  
RKLEGDSTDLSQDQIAELQQAQIAELKMQLAKKEELQAAALARVEEEAAQKNMALKKIRELESQISELQEDL  
ESERASRNKAEKQKRDILGEELEALKTELEDLTDSTAQQELRSKREQEVNILKKTLEEAKTHEAQIQEM  
RQKHSQAVEELAEQLEQTKRVKANLEKAKQTLENERGELANEVKVLLQKGKDSEHKRKKVEAQLQELQVK  
FNEGERVRTELADKVTKLQVELDNTGLLSQSDSKSSKLTDFSALESQQLQDTQELLQEENRQKLSLSTK  
LKQVEDEKNSFREQLEEEEAKHNLEKQIATLHAQVADMKKMEDSVGCLETAEEVKRKLQKDLEGLSQR

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HEEKVAAYDKLEKTKTRLQQELDDLLVDLDHQRSACNLEKKQKFQDQLLAEEKTISAKYAEERDRAEAE  
AREKETKALSLARALEEAMEQKAELERLNKQFRTEMEDLMSSKDDVGKSVHELEKSKRALLEQQVEEMKTQ  
LEELEDELOATEDAKLRLEVNLQAMKAQFERDLQGRDEQSEEKKQLVRQVREMEAELDERKQRSMAVA  
ARKKLEMDSLKDLEAHIDSANKRDEAIKQLRKQAMKDCMRELDTRASREEILAQAKENEKKLKSMEA  
EMIQLQEELAAAERAKRQAQQERDELADEIANSSGKGALALEEKRRLEARIAQLEEELEEEQGNTELIND  
RLKKANLQIDQINTDLNLERSHAQKNENARQQLERQNKELVKLQEMEGTVSKYKASITALEAKIAQLE  
EQLDNETKERQAACKQVRRTEKKLDVLLQVDDERRNAEQQYKDQADKASTRLKQLRKQLEEAEEEQRAN  
ASRRKLQRELEDATETADAMNREVSSLKNLRRGDLPPVVPRMARKGAGDGSDEEVDGKADGAEAKPAE

Calmodulin 2

GH1-84-PCR-G3F1 (SEQ ID NO:50)

GCTGTCTGAAATACCTGGTCTAACATCCCATGCCGCTCCCTCCTCACGATGCACCCACCGCCCTGAGGGCCCGTC  
CTAGGAATGGATGTGGGGATGGTCGTTGTAATGTGCTGGTCTCTTTTTCTTCCCCTTTGGCCCTTAA  
GACTTCATTGTTAGAACCAGTGGCTAGCTAAAGGGTGGGAGAGGGAAAGATGGGCCCCACACGCTCTCA  
AGAGAACGACCTGCAATAAACAGTCTTGCGGCCAGCTGCCAGGGACGGCAG

>gi|13477324|gb|BC005137.1|BC005137 Homo sapiens, calmodulin 2 (phosphorylase kinase, delta), clone MGC:1447 IMAGE:3504793, mRNA, complete cds (SEQ ID NO:51)

GGCACGAGGGCGCGGGAGCTGGAACGTGCTGCAGCTGCTGCCGCCGCCGGAGGAACCTTGATCCCCGTG  
CTCCGGACACCCCGGGCTCGCCATGGCTGACCAGCTGACTGAGGAGCAGATTGAGAGTTCAAGGAGGC  
CTTCTCCCTTTGACAAGGATGGAGATGGCACTATCACCACCAAGGAGTTGGGAGACTGATGAGATCC  
CTGGGACAGAACCCACTGAAGCAGACTGCAAGGATATGATCAATGAGGTGGATGCAGATGGAACGGGA  
CCATTGACTCCCGGAGTTCCCTGACCATGATGGCCAGAAAGATGAAGGACACAGACAGTGAGGAGGAGAT  
CCGAGAGGCGTCCGTGTTGACAAGGATGGAATGGCTACATCAGGCCAGAGCTGCGTCACGTA  
ATGACGAACCTGGGGAGAGCTGACCGATGAGGAGGTGGATGAGATGATCAGGGAGGCTGACATCGATG  
GAGATGGCCAGGTCAATTATGAAGAGTTGACAGATGACTGCAAAGTGAAGGCCCGGGCAGCT  
GGCGATGCCGTTCTCTGATCTCTCTCGCGCGCACTCTCTTCAACACTCCCCTGCGTACC  
CCGGTTCTAGCAAACACCAATTGATTGACTGAGAATCTGATAAAAGCAACAAAGATTGCCCCAGCTGC  
ATGATTGCTTTCTCCTTCCCTGAGTCTCTCCATGCCCTCATCTCTTCCCTTGCCTCGCCT  
CTTCCATCCATGTCTCCAAGGCCGTGATGCATTCAAAGTTGAAGCCCTCCCCAGATCCCCTGGGAGC  
CTCTGCCCTCCTCCAGGCCGGATGGCTCTCCATTTGGTTGTTCTTGTCTTGTCT  
TGGGTGCTGGGGTGGCTGCCAGCCCTGTCAGGGGGACCTGCTGGGAGGGACAAGAGGCCCTCCCCAGGCA  
GAAGAGCATGCCCTTGCGTTGCATGCAACCAGCCCTGTGATTCCACGTGAGATCCCAGCAGCCTGTT  
GGGGCAGGGTGCCAAGAGAGGCATTCCAGAAGGACTGAGGGGGCGTTGAGGAATTGTCGTTGACTGG  
ATGTGGCCAGGAGGGGTCGAGGGGGCAACTCACAGAAGGGGACTGACAGTGGCAACACTCACATCC  
CACTGGCTGCTGTTCTGAAACCATCTGATTGGCTTCTGAGGTTGGCTGGGTGGGACTGCTCATTGG  
CCACTCTGCAGATTGGACTTGCCCCGCTTCTGAAGCGCTCTCGAGCTGTTCTGTAATACCTGGTGTA  
ACATCCCCTGCCGCTCCCTCCTCACGATGCACCCACGCCCTGAGGGCCCTGAGGAATGGATGTGGG  
GATGGTCGCTTGTAAATGTGCTGGTTCTTTTTCTATGGCCCTTAAGACTTCATT  
TTGTTCAGAACCATGCTGGCTAGCTAAAGGGTGGGAGAGGAAGATGGGCCACACGCTCTCAAGA  
GAACGCACCTGCAATAAACAGTCTGCGCCAGCTGCCAGGGACGGCAGCTACAGCAGCCTCTGCG  
TCCCTGGTCCGCCAGCACCTCCCGCTCTCCGTGGTGAATTGGCGCCGCTTCTCACATCTGCTCCGTG  
CCCTCTCCCTGCCCTTCCCTGCCACCTGCCCTGCCCTACTCCCCAGCGGAGAGCATGATCCGT  
GCCCTTGCTCTGACTTCCGCTCTGGACAAGTAAGTCATGTGGCAGTCAGTCGCTGGGTTTT  
CCCCCTTCTGTTCAATTCTGAGGCTCCCTGGGACCTGCCAGCTTGTGAGAATCTTCTCATCCAC  
CTCACTGCCAGGTGATCAAGTGGCTTCTGGACAAGTGGGAGACCCAGCCAAGAGCTGAGGGT  
CCTCTGGCACCCAGCCCTGAGGAAGGAGGGATGGGCATAGTGGAGACCCAGCCAAGAGCTGAGGGT  
AAGGTCAAGGTAGGCAGTGGGAGGCTGAGGACATTTCGGAATGTTGGTTGTTTAAACCGGGCAA  
TATTGTGTTCAAGCTGTGAAGAAAAATATATCAATGTTCCAATAAAACAGTGAACACCT  
GAAAAAAAAAAAAAA

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>gi|13477325|gb|AAH05137.1|AAH05137 calmodulin 2 (phosphorylase kinase, delta) [Homo sapiens] (SEQ ID NO:52)  
MADQLTEEQIAEFKEAFSLFDKDGDTITKELGTVMSLQQNPEAELODMINEVDADGNGTIDFPEFL  
TMMARKMKDTDSEEEIREAFRVFDKGNGYISAAELRHVMTNLGEKLTDEEVDEMIREADIDGDGVNYE  
EFVQMMTAK

Novel Syporter

GH1-178-PCR-G3F1 (SEQ ID NO:53)

CTGGGTTCTGCGAGACTGGCTGGAGATCACGATGATGCCCTCACTGTCCAGTGAAACTCAAAACTCCATCACA  
GAGCCATCTCAATGCTCAAGTAGCGGCCCTCCCTGCCAGGCCGGCGACCCGAGTGGCGATCGCGGAGC  
AGGTCGGGCCAGAGGCCCTCCCTCCGAGGCTCTCACCTGCCACAGCCACCGCTGCACCGCAGGAACCCAGCA  
CAGTGGTTAGATTGATAAGCGGCCGCTCGACTAGTCTGAGGTCTGATACTCACTGACTGTCGTAT

Novel Semaphorin

GH1-204-PCR-G3F1 (SEQ ID NO:54)

AAAAAACTACTTCTAAGCTTGTCTTATTGTTGGCAGAATTCAAGGTCCCTGTGGCTGTAGGACCGAGGCCAGCT  
TCCCTGCTGATGTCGCTGGAGACTGCTGTCAGCTCCCAGAGGCCACCCCATCCTGGACACGTGCCCTCCATCT  
CAAACCTGCAGTGGGTGTTAACACCTCTCATGCTTCATCTACTTCAGGAATACAGATAGTGTCTGGTGGCTT  
GACGTGATTTAATGAATTGGACTCCATGTGGATTGGCTGCTCCCTATTCCGAGCTGCGGGCAGGGAGAGGGGC  
CTCGCGCCGCCCTCAGCAGCCGGCGCCGAGGTAGACGAGGGGACGGAAGGACAGACCGACGTGCCAGCTG  
GAATCATGTGAGGGCAACCAGGGAAAGGTGGAGCAGATGAGCACACAGGAGCCGCTCCCTACCGCCGCCCTCT  
CAGCATGGAACAGAGGCCCTGGCCCCGGCCCTGGAGGTGGACAGCCGCTCTGTGGCTGCT

Novel Zn finger helicase

GH1-31-PCR-G3F1 (SEQ ID NO:55)

GAAGGAGAAGATGGTATAAACTGGTCCATCAGTGACAAAGACATTGAGGCCAGATAGCTAATAACCGAACACCTGG  
AAGATGGACCAGCGGGTACTATTCAGCACAAAAACATTCTGAAATTGTGACAAACGTGGTATTTATCAAAA  
AACTGCCCTTACACAGAAAAGTCGCTGCTCCTGTGCTCCAGGAGAGGACATCTCTGTATTCTGTTCA  
CCCCCTTGCAGAATACTGCTGTGCTTAATGTTGACCACATGTCTTCAGACATTCTGGATAAACAGTGTG  
ACCGATGTCATATTGCTAGGCACATACAGATTCTGCCAGAAATCTTGAGGCAGTTATCACCTACGACAAACTTG  
ACCACCCAAAGCCAAAACCTTCCGAAAAACCCGACAGTGGTTGATTGATTAAGGCGGCCTGACTAGTCT  
GAGGTCTGATACTCACTGAC

Novel Sugar transporter

GH1-175-PCR-G3F1 (SEQ ID NO:56)

ACCGAGCCAGAGAATGTCACCAATGGCACAGTGGCGGCACAGCAGAGCCGGGCACGAGGAGGTGAGCTGGATGAA  
CGGCTGGCTCAGCTGCCAGGCCAGGACGAGATGCTAAATTGGCCTTCAGTGTGGCTCCTTGCTCAGGCCA  
TCACCCCTGCCCTGGGTATCGTCAAGTATGCCAGGAAGCTCAGGCTGCTGGCAGGCCCTGCTTCGCG  
GTTTCTGCTTGTGATTGCGT

human Plexin-A2 (SEQ ID NO:57)

gctgccggga ggagcggcat ccgcgccaga ctggagcggg agggcggcg aggca gtt  
ctggaaatt ttcagccgag agggcgacg atccggagag agaccccgag agcttggag  
cgttagggcg tgcagccgccc gcagccagcg gagcaaacct cgaatagat ctgaaagcc  
aggctcccg aggaaatggg actgtgaacg aacccggagag caagaaggg aggaagcc  
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tccgggtgcc ccctgagagc cggcgacagc gcccagccgg gctgctgccc ggcgacggag  
gactgagggg cgccggagc ggagaccggag gagcacttc aggaatacac agaatgtct  
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cattgactac tctgagaacc gcctgctgcc ctgtgggagc ctctaccagg gggtctgcaa  
gctgctgccc ctggatgacc tcttcatctt ggtggagcca tcccacaaga aggagacta  
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 gggagagaca gtggcgctcg tccatcctca gtgagaacac cagagaaccc gggggccggga  
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 cataggttttga gttcactcca atcatccagt ggtccctggc aatt

human Plexin-A2 (SEQ ID NO:58)

MEQRRPWPRALEVDSRSVVLSSVVWLLAPPAAGMPQFSTFHSENRDWTFNHLTvhQGTGAVYVGAINRVYKLTGNL  
 TIQVAHKTGPEEDNKSCYPPLIVQPCSEVLTLTNVNKLIIIDYSENRLACGSLYQGVCKLLRLLDILFILVEPSHK  
 KEHYLSSVNKTGTMGVIVRSEGEDGKLFIGTAVDGKQDYFPTLSSRKLPRDPESSAMLDYELHSDFVSSLIKIPSD  
 TLALVSHFDIFYIYGFASGGFVYFLTVQPETPEGVAINSAGDLFYTTSRIVRLCKDDPKFHSYVSLPFGCTRAVVEYR  
 LLQAAYLAKEPGDSLQAQAFNITSQDDVLFAIFSKGQKQYHHPPDDSSALCAFPIRAINLQIKERLQSCYQGEGLNLELNW  
 LLGKDQVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNGYSVVFVGTSGKLKKIRADG  
 PPHGGVQYEMVSVLKDGPILRDMAFSIDQRYLYVMSERQVTRVPVESCEQYTCGECLSSGDPHCGWCALHNCSR  
 RDKCQQAWEPNRFAASISQCVSLAVHPSSISVSEHSRLLSVSDAPDLASIACAFGNLTEVEGQVSGSQVICISP  
 GPKDVPVIPLDQDWGLELQLRSKETGKFVSTEFKFYNCSAHQCLLSCVNSAFRCHWCKYRNLC HDPTTCSFQEG  
 RINISEDCPQLVPTEEILIPVGEVKPITLKARNLPQPQSGQRGYECVLNIQGAIHRVPALRFNSSVQCQNSSYQD  
 GMDISNLAVDFAVVWNGNFIIDNPQDLKVHLYKCAAQRESCGLCLKADRKFECGWCSGERCTRLHQHCTSPSSPWLD  
 WSSHNVKCSNPQITEILTVSGPPEGGTRVTIHGVNLGLDFSEIAHHVQAVCPCTPLPGEYIIAEQIVCEMGHALVG  
 TTSGPVRLCIGECKPEFMKTSHQQYTFVNPSVLSLNPIRGPESGMTITGHYLGAGSSAVYLGQNTCEFYGRSM  
 SEIVCVSPSSNGLGPVPSVSVDRAHVDSNLQFEYIDDPRVQRIEPEWSIASGHTPLITGFNLDVIQEPRIRVKF  
 NGKESVNVCVKVNTTTLTCLAPSILTDYRPGLDTVERPDEFGFVNNVQSLIYNDTKIFIYPNPTFELLSPTGVLD  
 QKPGSPIILKGKNLCPPASGGAKLNYTTLIGETPCAVTSETQLCEPPNLTGQHKVMVHGGMFSPGSVSVISDS  
 LLTLPAVISIAAGGSLLLIVIIVLIAYKRKSRENDLTLKRLQMMDNLESRALECKEAFELQTDINELTSDLDR  
 SGIPYLDYRTYAMRVLPGIEDHPVLRERELEVQNGQQHVEKALKLFAQLINNKVFLLTFIRTLLELQRSFSMRDRGNV  
 ASLIMTGLQGRLEYATDVLKQLLSDLIDKNIENKNHPKLLRRTESVAEKMLTNWFafilHKFLKECAGEPLFMLYC  
 AIKQQMEKGPIADITGEARYSLSLEDKLIRQQIEYKTLILNCVNPDNENSPEIPVKVLCNTDTITQVKEKILDavyKNV  
 PYSPQRPRAVMDLEWRQGRIARVVLQDEDITTKIEGDWKRNLTMHYQVSDRSVALVPKQTSSYNIPASASISRTS  
 ISRYGDSSFRYTGSPDSLRSRAPMITPDLESQVKVWHLVKNHDHGDKEGDRGSKMVSEIYLTRLLATKGTLQKFVD  
 DLFETLFTVHRSALPLAIKYMDFLDEQADRHSIHDTDVRHTWKSNCPLRFWVNVIKNPQFVFDIHKGSITDAC  
 LSVVAQTFMDSCSTSEHRLGKDSPSNKLLYAKDIPSYKSWVERYYADIAKLPAISDQDMNAYLAEQSRLHAVEFNML  
 SALNEIYSYVSKYSEELIGALEQDEQARRQRLAYKVEQLINAMSIES

human deoxycytidylate deaminase (SEQ ID NO:59)

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ccggaatccg agatagggtt gcacatctgt cctgacacagac gaggagtgtt actgaaccag  
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taccaatatt attaaaatct tattaaaatc t

human deoxycytidylate deaminase (SEQ ID NO:60)

MSEVSCKRDDYLEWPEYFMAVAFLSAQRSKDPNSQVGACIVNSENKIVGIGYNGMPNGCSDDVLPWRRTAENKLDTKPYVCHAELNAINMNKNSTDVKGCSMYVALFPCNECAKLI IQAGIKEVIFTSDKYHDSDEATAARLLFNMAGVTFRKFIPKCSKIVIDFDSINSRPSQKLÖ--

Please insert the accompanying paper copy of the Sequence Listing, page numbers 1-103, at the end of the application.